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More specifically, outlined below is a description as
to how an artisan would have utilized the information
provided in the subject application, together with
technologies and information readily available at the time
of filing, to practice the claimed invention.[1]  (DDRT 16 is
used by way of Example.)

1.    The nucleotide sequence of clone DDRT16 is given
in Figure 5 of the application (SEQ ID NO:40). (GenBank
accession number, AF071356).  (See attached Figures 1 and
2.)

2.    The nucleotide sequence for DDRT16 can be
analyzed using the general nucleotide sequence database and
the program BLASTN, which compares nucleotide to nucleotide
sequences.  (The results of this analysis show that the
nucleotide sequence of DDRT16 is identical to itself and
that of the *C. elegans* cosmid F35E8.)  The results of this
analysis are shown in attached Figure 3.  This analysis

---

[1] All of the programs referenced above are available via the Internet or
can be downloaded, free of charge.

For the Examiner's ease of access, the following are provided:

The URL for the Entrez server is: http://www.ncbi.nlm.nih.gov/Entrez/

The URL of the GenBank BLAST server is
http://www.ncbi.nlm.nih.gov:80/BLAST/

The URL of the *C. elegans* BLAST server is:
http://www.sanger.ac.uk/Projects/C_elegans/blast_server.shtml

A description of ACeDb can be found at: http://www.acedb.org/

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provides access to the complete genomic sequence of the

gene that encoded DDRT16.  By entering the accession number

for F35E8, 2653095 (see Figure 3), the nucleotide sequence

for this cosmid can be obtained.

3.    The nucleotide sequence for DDRT16 can be

analyzed using the program BLASTN and the *C. elegans*

specific genomic nucleotide sequence database.  (The

results of this analysis show that the nucleotide sequence

of DDRT16 is identical to the *C. elegans* cosmid F35E8.)

The results of this analysis are shown in attached

Figure 4.  This analysis provides access to the complete

genomic sequence of the gene that encoded DDRT16.  By

entering the accession number for F35E8, 2653095, the

nucleotide sequence for this cosmid can be obtained.

4.    The nucleotide sequence for DDRT16 can be

analyzed using the *C. elegans* predicted protein amino acid

sequence database and the program BLASTX, which compares

translated nucleotide sequences to amino acid sequences.

(The result of this analysis shows that the protein encoded

by the nucleotide sequence of DDRT16 is identical to the

predicted *C. elegans* protein F35E8.11.)  The results of

this analysis are shown in attached Figure 5.  This

analysis provides access to the complete protein sequence

of the DDRT16.

5.   To obtain the complete sequences for the mRNA and

protein, the program AceDb can be used.   ACeDb is a C.

elegans specific database that contains all of the

information related to the C. elegans genome.   It includes

the entire genomic sequence, sequences for the predicted

mRNAs, cDNAs and proteins.   The data that are presented

include introns/exon locations and can be used to identify

the regulatory/promoter regions of genes.   By searching for

F35E8.11 in AceDb, the map of the intron/exon structure,

and the cDNA and protein sequences can be obtained (see

attached Figures 6-8).

6.   By searching for F35E8 in ACeDb, the entire

nucleotide sequence for this cosmid can be obtained.   By

knowing the start codon for F35E8.11 and the location of

the adjacent gene, the regulatory region/promoter for this

gene can be predicted.

Summarizing, given the accession number for the

sequence data provided in the application, any person with

minimal molecular biology experience can readily obtain the

complete gene, mRNA and protein sequences, using freely

available, user-friendly programs and data analysis

software available via the Internet.   Accordingly, it

should be clear that Applicants had full possession of the

claimed invention at the time of filing and further that

the disclosure provided is enabling.  Reconsideration is

thus requested.

This application is submitted to be in condition for

allowance and a Notice to that effect is requested.

Respectfully submitted,

**NIXON & VANDERHYE, P.C.**

By _____
Mary J. Wilson
Reg. No. 32,955

MJW:tat

1100 North Glebe Road, 8th Floor
Arlington, Virginia 22201-4714
Telephone:  (703) 816-4000
Facsimile:  (703) 816-4100

**NCBI**          _Nucleotide_

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM |

Search Nucleotide ▼ for AF071356    Go | Clear

Limits      Preview/Index      History      Clipboard

Display | Summary ▼ | Save | Text | Details | Add to Clipboard

☐ 1: AF071356                             PubMed, Taxonomy

AF071356 mRNA from cadmium-responsive gene Caenorhabditis elegans
cDNA clone DDRT16, mRNA sequence
gi|3265101|gb|AF071356.1|AF071356[3265101]

Revised: March 12, 2001.

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

# Figure 2

## NCBI — Nucleotide

| PubMed | Nucleotide | Protein | Genome | Structure | PopSet | Taxonomy | OMIM |

Search Nucleotide for [                    ] Go | Clear

Limits     Index     History     Clipboard

Display  Default View  as  HTML  Save  Add to Clipboard

☐ 1: AF071356  AF071356 mRNA from cadmium-responsive gene            PubMed, Taxonomy, LinkOut
Caenorhabditis elegans cDNA clone DDRT16, mRNA
sequence

**IDENTIFIERS**

| | |
|---|---|
| dbEST Id: | 1777139 |
| EST name: | AF071356 |
| GenBank Acc: | AF071356 |
| GenBank gi: | 3265101 |

**CLONE INFO**

| | |
|---|---|
| Clone Id: | DDRT16 |
| DNA type: | cDNA |

**PRIMERS**

| | |
|---|---|
| PolyA Tail: | Unknown |

**SEQUENCE**

```
TTTTTTTTTTTTTGGGAGGAAATCACGGCGGCGGATGCAACAGTCTTCTCTCAATTGGCA
ACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAG
TTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGA
ATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCAAAAAAAAAAAA
```

| | |
|---|---|
| Entry Created: | Jun 30 1998 |
| Last Updated: | Nov 25 1998 |

**LIBRARY**

| | |
|---|---|
| Lib Name: | mRNA from cadmium-responsive gene |
| Organism: | Caenorhabditis elegans |
| Strain: | N2 |
| Tissue type: | whole animal |
| Develop. stage: | mixed population |

**SUBMITTER**

| | |
|---|---|
| Name: | Jonathan H. Freedman |
| Lab: | Nicholas School of the Environment |
| Institution: | Duke University |
| Address: | Box 90328, Durham, NC 27708-0328, USA |
| E-mail: | jonf@duke.edu |

**CITATIONS**

| | |
|---|---|
| Medline UID: | 99041962 |
| Title: | Cadmium-regulated genes from the nematode Caenorhabditis elegans. Identification and cloning of new cadmium-responsive genes by differential display |
| Authors: | Liao,V.H.-C., Freedman,J.H. |
| Citation: | J. Biol. Chem. 273 (48): 31962-70 1998 |

**MAP DATA**

# Figure 3

## ᘒ NCBI        *results* of **BLAST**

**BLASTN 2.1.3 [Apr-11-2001]**

RID: 990026953-3242-12725

Query= gi|3265101|gb|AF071356.1|AF071356 AF071356 mRNA from
cadmium-responsive gene Caenorhabditis elegans cDNA clone DDRT16, mRNA
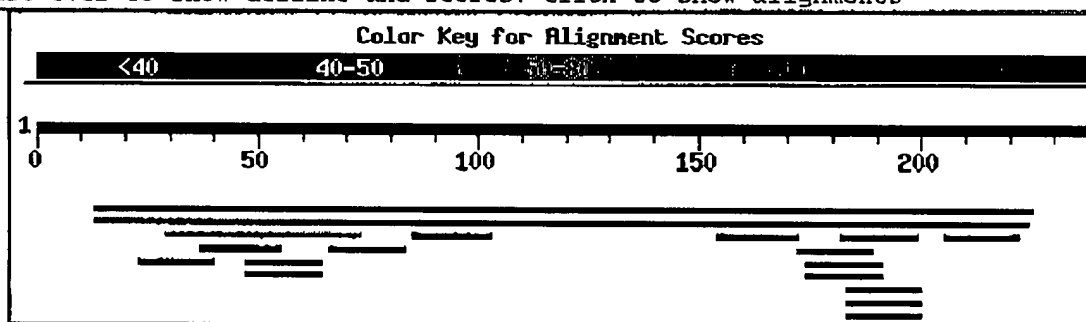sequence
        (238 letters)

Database: nt
          861,799 sequences; 3,247,139,289 total letters

If you have any problems or questions with the results of this search
please refer to the **BLAST FAQs**

Taxonomy reports

## Distribution of 19 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



| Sequences producing significant alignments: | Score (bits) | E Value |
|---|---|---|
| gi|11120428|gb|AF301606.1|AF301606  Caenorhabditis elegans c... | 422 | e-116 |
| gi|2653095|emb|Z81529.1|CEF35E8  Caenorhabditis elegans cosm... | 381 | e-103 |
| gi|1418539|emb|Z75543.1|CEK01D12  Caenorhabditis elegans cos... | 50 | 6e-04 |
| gi|12620418|gb|AF322012.1|AF322012S1  Bradyrhizobium japonic... | 38 | 2.3 |
| gi|4982441|gb|AE001823.1|AE001823  Thermotoga maritima secti... | 38 | 2.3 |
| gi|1627880|emb|Z81074.1|CEF32B6  Caenorhabditis elegans cosm... | 38 | 2.3 |
| gi|12583776|gb|AC010585.6|AC010585  Homo sapiens chromosome ... | 36 | 9.0 |
| gi|10727249|gb|AE003475.2|AE003475  Drosophila melanogaster ... | 36 | 9.0 |
| gi|7301915|gb|AE003773.1|AE003773  Drosophila melanogaster g... | 36 | 9.0 |
| gi|10043285|gb|AC003046.3|AC003046  Homo sapiens Xp22 PACs R... | 36 | 9.0 |

```
gi|6598428|gb|AC004665.2|AC004665   Arabidopsis thaliana chro...   36   9.0
gi|6409187|gb|AF145126.1|DRMFER2    Drosophila melanogaster fe...  36   9.0
gi|3212170|gb|AF001905.1|AF001905   Homo sapiens cosmids E079...   36   9.0
gi|11229166|emb|AL357892.13|AL357892  Human DNA sequence fro...    36   9.0
gi|5531462|emb|AL096851.1|SPBC1105  S.pombe chromosome II co...    36   9.0
gi|1301745|emb|Z72519.1|HSJ13817A   Human DNA sequence from c...   36   9.0
gi|7768698|dbj|AP001686.1|AP001686  Homo sapiens genomic DNA...    36   9.0
gi|7077191|dbj|AP001255.1|AP001255  Homo sapiens genomic DNA...    36   9.0
```

**Alignments**

>gi|11120428|gb|AF301606.1|AF301606 Caenorhabditis elegans cadmium-inducible lysosomal ⸏
       (cdr-1) mRNA, complete cds
       Length = 907

 Score = 422 bits (213), Expect = e-116
 Identities = 213/213 (100%)
 Strand = Plus / Plus

```
Query:  14  gggaggaaatcacggcggcggatgcaacagtcttctctcaattggcaactgtctattatc  73
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683  gggaggaaatcacggcggcggatgcaacagtcttctctcaattggcaactgtctattatc  742


Query:  74  cattccgcaatcacatttcggatgttctcgaaaaggacttcccaaagttattggagtact  133
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743  cattccgcaatcacatttcggatgttctcgaaaaggacttcccaaagttattggagtact  802


Query: 134  gtgaaagagttcgtcatgaagtttacccaaaggactttactatgtgaattaaattgtcaa  193
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803  gtgaaagagttcgtcatgaagtttacccaaaggactttactatgtgaattaaattgtcaa  862


Query: 194  actagtagtcagatcaataaaattctacgtggc  226
            |||||||||||||||||||||||||||||||||
Sbjct: 863  actagtagtcagatcaataaaattctacgtggc  895
```

>gi|2653095|emb|Z81529.1|CEF35E8 Caenorhabditis elegans cosmid F35E8, complete sequence
       Length = 23602

 Score = 381 bits (192), Expect = e-103
 Identities = 195/196 (99%)
 Strand = Plus / Plus

```
Query:  30    ggcggatgcaacagtcttctctcaattggcaactgtctattatccattccgcaatcacat  89
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18625  ggcggatgcaacagtcttctctcaattggcaactgtctattatccattccgcaatcacat  18684


Query:  90    ttcggatgttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcgtca  149
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18685  ttcggatgttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcgtca  18744


Query: 150    tgaagtttacccaaaggactttactatgtgaattaaattgtcaaactagtagtcagatca  209
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18745  tgaagtttacccaaaggactttactatgtgaattaaattgtcaaactagtagtcagatca  18804


Query: 210    ataaaattctacgtgg  225
              |||||||| |||||||
```

```
gi|6598428|gb|AC004665.2|AC004665    Arabidopsis thaliana chro...    36    9.0
gi|6409187|gb|AF145126.1|DRMFER2     Drosophila melanogaster fe...   36    9.0
gi|3212170|gb|AF001905.1|AF001906    Homo sapiens cosmids E079...    36    9.0
gi|11229166|emb|AL357892.13|AL357892 Human DNA sequence fro...       36    9.0
gi|5531462|emb|AL096851.1|SPBC1105   S.pombe chromosome II co...     36    9.0
gi|1301745|emb|Z72519.1|HSJ13817A    Human DNA sequence from c...    36    9.0
gi|7768698|dbj|AP001686.1|AP001686   Homo sapiens genomic DNA...     36    9.0
gi|7077191|dbj|AP001255.1|AP001255   Homo sapiens genomic DNA...     36    9.0
```

**Alignments**

>gi|11120428|gb|AF301606.1|AF301606 Caenorhabditis elegans cadmium-inducible lysosomal p
        (cdr-1) mRNA, complete cds
        Length = 907

 Score = 422 bits (213), Expect = e-116
 Identities = 213/213 (100%)
 Strand = Plus / Plus

```
Query:  14  gggaggaaatcacggcggcggatgcaacagtcttctctcaattggcaactgtctattatc  73
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 683  gggaggaaatcacggcggcggatgcaacagtcttctctcaattggcaactgtctattatc  742

Query:  74  cattccgcaatcacatttcggatgttctcgaaaaggacttcccaaagttattggagtact  133
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 743  cattccgcaatcacatttcggatgttctcgaaaaggacttcccaaagttattggagtact  802

Query: 134  gtgaaagagttcgtcatgaagtttacccaaaggactttactatgtgaattaaattgtcaa  193
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 803  gtgaaagagttcgtcatgaagtttacccaaaggactttactatgtgaattaaattgtcaa  862

Query: 194  actagtagtcagatcaataaaattctacgtggc  226
            |||||||||||||||||||||||||||||||||
Sbjct: 863  actagtagtcagatcaataaaattctacgtggc  895
```

>gi|2653095|emb|Z81529.1|CEF35E8 Caenorhabditis elegans cosmid F35E8, complete sequence
        Length = 23602

 Score = 381 bits (192), Expect = e-103
 Identities = 195/196 (99%)
 Strand = Plus / Plus

```
Query:   30    ggcggatgcaacagtcttctctcaattggcaactgtctattatccattccgcaatcacat  89
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18625  ggcggatgcaacagtcttctctcaattggcaactgtctattatccattccgcaatcacat  18684

Query:   90    ttcggatgttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcgtca  149
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18685  ttcggatgttctcgaaaaggacttcccaaagttattggagtactgtgaaagagttcgtca  18744

Query:  150    tgaagtttacccaaaggactttactatgtgaattaaattgtcaaactagtagtcagatca  209
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18745  tgaagtttacccaaaggactttactatgtgaattaaattgtcaaactagtagtcagatca  18804

Query:  210    ataaaattctacgtgg  225
               |||||||| |||||||
```

```
Sbjct: 18805 ataaaattttacgtgg 18820

 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Plus


Query: 14      gggaggaaatcacggcgg 31
               ||||||||||||||||||
Sbjct: 18556 gggaggaaatcacggcgg 18573
```

>gi|1418539|emb|Z75543.1|CEK01D12 Caenorhabditis elegans cosmid K01D12, complete sequenc
            Length = 36974

```
 Score - 50.1 bits (25), Expect = 6e-04
 Identities = 40/45 (88%)
 Strand = Plus / Minus


Query: 30      ggcggatgcaacagtcttctctcaattggcaactgtctattatcc 74
               |||||||||||||| ||  |||||||||||| |||||||
Sbjct: 31282 ggcggatgcaacagtgtttggtcaattggcaactgtatattatcc 31238
```

>gi|12620418|gb|AF322012.1|AF322012S1 Bradyrhizobium japonicum symbiotic gene region, pa
            Length = 180000

```
 Score = 38.2 bits (19), Expect = 2.3
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query: 155     tttacccaaaggactttac 173
               |||||||||||||||||||
Sbjct: 57778 tttacccaaaggactttac 57760
```

>gi|4982441|gb|AE001823.1|AE001823 Thermotoga maritima section 135 of 136 of the complet
            Length = 12762

```
 Score = 38.2 bits (19), Expect = 2.3
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query: 86      acatttcggatgttctcga 104
               |||||||||||||||||||
Sbjct: 5927 acatttcggatgttctcga 5909
```

>gi|1627880|emb|Z81074.1|CEF32B6 Caenorhabditis elegans cosmid F32B6, complete sequence
            Length = 27394

```
 Score = 38.2 bits (19), Expect = 2.3
 Identities = 19/19 (100%)
 Strand = Plus / Minus


Query: 38      caacagtcttctctcaatt 56
               |||||||||||||||||||
Sbjct: 21939 caacagtcttctctcaatt 21921
```

>gi|12583776|gb|AC010585.6|AC010585 Homo sapiens chromosome 5 clone CTC-315O24, complete
            Length = 174882

```
 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
```

Strand - Plus / Minus


Query: 173     ctatgtgaattaaattgt 190
               ||||||||||||||||||
Sbjct: 53097   ctatgtgaattaaattgt 53080


>gi|10727249|gb|AE003475.2|AE003475 Drosophila melanogaster genomic scaffold 14200001338
          complete sequence
          Length = 300829

 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query: 24      cacggcggcggatgcaac 41
               ||||||||||||||||||
Sbjct: 163288  cacggcggcggatgcaac 163271


>gi|7301915|gb|AE003773.1|AE003773 Drosophila melanogaster genomic scaffold 14200001338
          105, complete sequence
          Length = 226905

 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query: 175     atgtgaattaaattgtca 192
               ||||||||||||||||||
Sbjct: 183441  atgtgaattaaattgtca 183424


>gi|10043285|gb|AC003046.3|AC003046 Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 c
          Length = 166758

 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query: 206     atcaataaaattctacgt 223
               ||||||||||||||||||
Sbjct: 104081  atcaataaaattctacgt 104064


>gi|6598428|gb|AC004665.2|AC004665 Arabidopsis thaliana chromosome II section 244 of 255
          sequence. Sequence from clones F17K2, P4I18
          Length = 89794

 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Plus


Query: 183     taaattgtcaaactagta 200
               ||||||||||||||||||
Sbjct: 27994   taaattgtcaaactagta 28011


>gi|6409187|gb|AF145126.1|DRMFER2 Drosophila melanogaster ferritin gene cluster
          Length = 3066

 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus

```
Query: 175 atgtgaattaaattgtca 192
            ||||||||||||||||||
Sbjct: 719 atgtgaattaaattgtca 702
```

>gi|3212170|gb|AF001905.1|AF001905 Homo sapiens cosmids E079, B0920 and A8 from Xq25 X-]
            lymphoproliferative disease gene candidate region,
            complete sequence
            Length = 197620

```
 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus
```

```
Query: 48    ctctcaattggcaactgt 65
             ||||||||||||||||||
Sbjct: 94392 ctctcaattggcaactgt 94375
```

>gi|11229166|emb|AL357892.13|AL357892 Human DNA sequence from clone RP11-707H15 on chron
            sequence [Homo sapiens]
            Length = 189876

```
 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Plus
```

```
Query: 184    aaattgtcaaactagtag 201
              ||||||||||||||||||
Sbjct: 148220 aaattgtcaaactagtag 148237
```

>gi|5531462|emb|AL096851.1|SPBC1105 S.pombe chromosome II cosmid c1105
            Length = 34982

```
 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Plus
```

```
Query: 67    tattatccattccgcaat 84
             ||||||||||||||||||
Sbjct: 16858 tattatccattccgcaat 16875
```

>gi|1301745|emb|Z72519.1|HSJ13817A Human DNA sequence from cosmid J138017, between marke
            DXS8038 on chromosome X contains EST CA repeat and an
            endogenous retroviral like element
            Length = 125787

```
 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus
```

```
Query: 48    ctctcaattggcaactgt 65
             ||||||||||||||||||
Sbjct: 94392 ctctcaattggcaactgt 94375
```

>gi|7768698|dbj|AP001686.1|AP001686 Homo sapiens genomic DNA, chromosome 21q, section 3(
            Length = 340000

```
 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
```

```
Strand = Plus / Minus


Query: 184    aaattgtcaaactagtag 201
              ||||||||||||||||||
Sbjct: 280556 aaattgtcaaactagtag 280539


>gi|7077191|dbj|AP001255.1|AP001255 Homo sapiens genomic DNA, chromosome 21q21.1-q21.2,
          LL56-APP region, complete sequence
        Length - 83921

 Score = 36.2 bits (18), Expect = 9.0
 Identities = 18/18 (100%)
 Strand = Plus / Minus


Query: 184    aaattgtcaaactagtag 201
              ||||||||||||||||||
Sbjct: 50434  aaattgtcaaactagtag 50417

  Database: nt
    Posted date:  May 11, 2001  4:10 AM
  Number of letters in database: -1,072,656,299
  Number of sequences in database:  858,416


Lambda     K        H
    1.37    0.711    1.31

Gapped
Lambda     K        H
    1.37    0.711    1.31


Matrix: blastn matrix:1 -3
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 355216
Number of Sequences: 858416
Number of extensions: 355216
Number of successful extensions: 26098
Number of sequences better than 10.0: 18
length of query: 238
length of database: 3,222,310,993
effective HSP length: 19
effective length of query: 219
effective length of database: 3,206,001,089
effective search space: 702114238491
effective search space used: 702114238491
T: 0
A: 30
X1: 6 (11.9 bits)
X2: 15 (29.7 bits)
S1: 12 (24.3 bits)
S2: 18 (36.2 bits)
```

# Figure 4

Intranet | Sanger Centre | Acedb | Acebrowser | Ensembl | Trace Server | Library
Info | Database Searches | HGP | Projects | Software | Teams | Search

**The Sanger Centre**

Data Release Policy | Conditions of Use

## Blast Server Results

*powered by*
**COMPAQ** *NonStop*

**Low complexity filtering disabled**
**Repeatmasker disabled**

```
BLASTN 2.0a13MP-WashU [10-Jun-1997] [Build 23:08:16 Jun 10 1997]

Reference:  Gish, Warren (1994-1997).  unpublished.
Altschul, Stephen F., Warren Gish, Webb Miller, Eugene W. Myers, and David J.
Lipman (1990).  Basic local alignment search tool.  J. Mol. Biol. 215:403-10.

Notice:  this program and its default parameter settings are optimized to find
nearly identical sequences rapidly.  To identify weak similarities encoded in
nucleic acid, use BLASTX, TBLASTN or TBLASTX.

Query= gi
       (238 letters)

Database:  wormpub/allcmid
           3692 sequences; 104,258,147 total letters.
Searching....10....20....30....40....50....60....70....80....90....100% done
```

|  |  | High | Smallest Sum Probability | |
|---|---|---|---|---|
| Sequences producing High-scoring Segment Pairs: | | Score | P(N) | N |
| F35E8 | ACC=Z81529 | 971 | 8.1e-38 | 1 |
| K01D12 | ACC=Z75543 | 451 | 2.6e-14 | 1 |
| C54D10 | ACC=Z75531 | 451 | 2.6e-14 | 1 |
| C07A4 | ACC=Z78536 | 163 | 0.24 | 1 |
| Y71G12B | ACC=AC025726 | 143 | 0.39 | 2 |
| Y49F6A | ACC=AC024800 | 153 | 0.53 | 1 |
| F54B3 | ACC=Z48583 | 152 | 0.57 | 1 |
| C03A7 | ACC=AF016451 | 152 | 0.57 | 1 |
| ZK287 | ACC=Z70757 | 149 | 0.69 | 1 |
| Y22D7AL | ACC=AC084153 | 147 | 0.76 | 1 |
| Y11D7A | ACC=AL032632 | 146 | 0.80 | 1 |
| C46E10 | ACC=AF039710 | 145 | 0.83 | 1 |
| F23H11 | ACC=AF003389 | 144 | 0.86 | 1 |
| T24C4 | ACC=AF100306 | 144 | 0.86 | 1 |
| Y53H1A | ACC=AL132864 | 143 | 0.89 | 1 |
| T07C12 | ACC=Z73976 | 143 | 0.89 | 1 |
| B0285 | ACC=Z34533 | 143 | 0.89 | 1 |
| F10G2 | ACC=U64836 | 142 | 0.91 | 1 |
| Y48G1A | ACC=AC024792 | 142 | 0.91 | 1 |
| F56G4 | ACC=Z81552 | 141 | 0.93 | 1 |
| W03B1 | ACC=U58753 | 141 | 0.93 | 1 |
| Y48A6B | ACC=AL023844 | 141 | 0.93 | 1 |

| T24C12 | ACC=U41037 | | 140 | 0.95 | 1 |
| F21D5 | ACC=Z54271 | | 140 | 0.95 | 1 |
| Y54B5A | ACC=AL032643 | | 140 | 0.95 | 1 |
| Y47D3A | ACC=AL117202 | | 140 | 0.95 | 1 |
| ZK675 | ACC=Z46812 | | 138 | 0.97 | 1 |
| ZK1025 | ACC=AL022288 | | 138 | 0.97 | 1 |
| D1065 | ACC=AF016414 | | 137 | 0.98 | 1 |
| LLC1 | ACC=Z82277 | | 137 | 0.98 | 1 |
| Y71F9AR | ACC=AC024853 | | 137 | 0.98 | 1 |
| Y53F4B | ACC=AL132949 | | 137 | 0.98 | 1 |
| R10E11 | ACC=Z29095 | | 136 | 0.9999 | 1 |
| F43C1 | ACC=Z46937 | | 136 | 0.9999 | 1 |
| C44H4 | ACC=Z79598 | | 136 | 0.9999 | 1 |

>F35E8 [Full Sequence]　　[AceBrowser]　　ACC=Z81529
　　　　Length = 23,602

　Plus Strand HSPs:

　Score = 971 (145.7 bits), Expect = 8.1e-38, P = 8.1e-38
　Identities = 195/196 (99%), Positives = 195/196 (99%), Strand = Plus / Plus

Query:　　30 GGCGGATGCAACAGTCTTCTCTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACAT 89
　　　　　　 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18625 GGCGGATGCAACAGTCTTCTCTCAATTGGCAACTGTCTATTATCCATTCCGCAATCACAT 18684

Query:　　90 TTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCA 149
　　　　　　 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18685 TTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCA 18744

Query:　 150 TGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAAATTGTCAAACTAGTAGTCAGATCA 209
　　　　　　 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 18745 TGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAAATTGTCAAACTAGTAGTCAGATCA 18804

Query:　 210 ATAAAATTCTACGTGG 225
　　　　　　 ||||||||| |||||||
Sbjct: 18805 ATAAAATTTTACGTGG 18820

　Score = 145 (21.8 bits), Expect = 1.8, P = 0.83
　Identities = 47/65 (72%), Positives = 47/65 (72%), Strand = Plus / Plus

Query:　　 4 TTTTTTTTTTGGGAGGAAATCACGGCGGCGGATGCAACAGTCTTCTCTCAATTGGCAACT 63
　　　　　　 TTT TTTT GGGAGGAAATCACGGCGG  AT CA CAGTCT T    AATTG  A CT
Sbjct: 18546 TTTCTTTTCGGGGAGGAAATCACGGCGGTAAATACA-CAGTCTAATAA-AATTGT-ATCT 18602

Query:　　 64 GTCTA 68
　　　　　　 G C A
Sbjct: 18603 GGCAA 18607

>K01D12 [Full Sequence]　　[AceBrowser]　　ACC=Z75543
　　　　Length = 36,974

　Minus Strand HSPs:

　Score = 451 (67.7 bits), Expect = 2.6e-14, P = 2.6e-14
　Identities = 157/231 (67%), Positives = 157/231 (67%), Strand = Minus / Plus

Query:　 235 TTTTTTTTTGCCACGTAGAATTTTATTGATCTGACTACTAGTTTGACAATTTAAT-TCAC 177
　　　　　　 TTTTT  TG CACG A  A TTTATT  TC A  A T     A AAT A T TCA

```
Sbjct:  34627  TTTTTCAGTGTCACG-ATTAGTTTATT--TCAAAAAAGTTACCGCATAATACATTCTCAA 34683

Query:   176   ATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACTCCAATAACTTT 117
               ATAGTAAA TC TTTGG TAAA TTC T  CG A TCTTTCACAGTACT  A  A CTTT
Sbjct:  34684  ATAGTAAAATCATTTGGATAAATTTCCTTTCGGATTCTTTCACAGTACTGTAGAATCTTT 34743

Query:   116   GGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAATGGATAATAGACAGTTGCC 57
               GGGAA TC TTTTC AGAACA   GA ATGTGA TG   AATGGATAATA ACA  TGCC
Sbjct:  34744  GGGAAATCATTTTCAAGAACAGTAGAGATGTGAGTGTAAAATGGATAATAAACAACTGCC 34803

Query:    56   AATTGAGAGAAGACTGTTGCATCCGCCGCCGTGATTTCCTC-CCAAAAAAAAA 5
               AA TG   AA AC GT GCATC  C G  AT T  TC CCAAA AAA A
Sbjct:  34804  AACTGGCTAAAAACCGTCGCATCAACTGGAGCAATGTGGTCTCCAAATAAATA 34856


  Score = 421 (63.2 bits), Expect = 6.0e-13, P = 6.0e-13
  Identities = 123/166 (74%), Positives = 123/166 (74%), Strand = Minus / Plus

Query:   195   GTTTGACAATTTAATTCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTC 136
               GTTT A AA T AATTCA AT GTAAA TC TT GG TA A TTC T  CG ACTCTTTC
Sbjct:  31118  GTTTCAAAAAT-AATTCAAATTGTAAAATCGTTAGGATAGATTTCTTTGCGTACTCTTTC 31176

Query:   135   ACAGTACTCCAATAACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAA 76
                A TA TC A  A CTT GGGAA TC TT TC AGAACATC G  A TGA   CG AA
Sbjct:  31177  CAAATATTCAAGCACCTTGGGGAAATCTTTGTCAAGAACATCGGTCAGATGAGAACG-AA 31235

Query:    75   T-GGATAATAGACAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCC 30
               T GGATAATA ACAGTTGCCAATTGA   AA ACTGTTGCATCCGCC
Sbjct:  31236  TAGGATAATATACAGTTGCCAATTGACCAAACACTGTTGCATCCGCC 31282




>C54D10 [Full Sequence]  [AceBrowser]    ACC=Z75531
        Length = 40,450


    Minus Strand HSPs:

  Score = 451 (67.7 bits), Expect = 2.6e-14, P = 2.6e-14
  Identities = 157/231 (67%), Positives = 157/231 (67%), Strand = Minus / Plus

Query:   235   TTTTTTTTTGCCACGTAGAATTTTATTGATCTGACTACTAGTTTGACAATTTAAT-TCAC 177
               TTTTT  TG CACG A A TTATT  TC  A T     A AAT A T TCA
Sbjct:   1867  TTTTTGAGTGTCACG-ATTAGTTTATT--TCAAAAAAGTTACCGCATAATACATTCTCAA 1923

Query:   176   ATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACTCCAATAACTTT 117
               ATAGTAAA TC TTTGG TAAA TTC T  CG A TCTTTCACAGTACT  A  A CTTT
Sbjct:   1924  ATAGTAAAATCATTTGGATAAATTTCCTTTCGGATTCTTTCACAGTACTGTAGAATCTTT 1983

Query:   116   GGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAATGGATAATAGACAGTTGCC 57
               GGGAA TC TTTTC AGAACA   GA ATGTGA TG   AATGGATAATA ACA  TGCC
Sbjct:   1984  GGGAAATCATTTTCAAGAACAGTAGAGATGTGAGTGTAAAATGGATAATAAACAACTGCC 2043

Query:    56   AATTGAGAGAAGACTGTTGCATCCGCCGCCGTGATTTCCTC-CCAAAAAAAAA 5
               AA TG   AA AC GT GCATC  C G  AT T  TC CCAAA AAA A
Sbjct:   2044  AACTGGCTAAAAACCGTCGCATCAACTGGAGCAATGTGGTCTCCAAATAAATA 2096


  Score = 352 (52.8 bits), Expect = 7.8e-10, P = 7.8e-10
  Identities = 122/178 (68%), Positives = 122/178 (68%), Strand = Minus / Plus

Query:   183   AATTCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACTCCAA 124
               AATT A AT GTAAA TC TTTGG TA A TTC TGACGAACTC TTCACA TA TCCA
Sbjct:   5615  AATTAA-ATTGTAAAATCATTTGGATATATTTCCTGACGAACTCGTTCACAATATTCCAG 5673
```

```
Query:    123 TAACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATG-TGATTGCGGAATGGATAATAGA 65
                A TTTGGGAA TC TTTTC AG CATC   AT TG   CGGAATGGATAA   A
Sbjct:   5674 AATTTTTGGGAAATCATTTTCAAGGGCATCGTTGATACTGCAC-CGGAATGGATAAATCA 5732

Query:     64 CAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCCGCCGTGATTTCCTCCCAAAAAAAA 6
                C G  GC A TTGA   AA AC G TGCATC GCC   G ATTT  T  A AAAAAA
Sbjct:   5733 CCGACGCAATTTGACCAAATACAGCTGCATCTGCCT--GAAATTTTATGAGATAAAAAA 5789


   Score = 296 (44.4 bits), Expect = 2.7e-07, P = 2.7e-07
   Identities = 110/162 (67%), Positives = 110/162 (67%), Strand = Minus / Plus

Query:    191 GACAATTTAATTCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAG 132
                GA AA TTA TTCA A A  AAA TC TTTGG TAAA  TC T  CGAAC C  TC CA
Sbjct:   7285 GAAAAGTTA-TTCA-ACA--AAA-TCATTTGGATAAATCTCTTTGCGAACACGCTCGCAA 7339

Query:    131 TACTCCAATAACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAATGGA 72
                TA TCCA A CT GG AA TC TTTC AGAA ATC   AAT T   GCGGAATGGA
Sbjct:   7340 TATTCCAGAAGCTGAGGAAAATCATTTTCCAGAATATCGTTAATTTTGCAGCGGAATGGA 7399

Query:     71 TAA-TAGACAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCC 30
                TAA TA AC GT GC A TTG   AA ACTG TGC TC GCC
Sbjct:   7400 TAAATA-ACTGTGGCGAGTTGTCCAAAAACTGCTGCGTCTGCC 7441



>C07A4 [Full Sequence]  [AceBrowser]   ACC=Z78536
       Length = 16,878


   Minus Strand HSPs:


   Score = 163 (24.5 bits), Expect = 0.27, P = 0.24
   Identities = 135/220 (61%), Positives = 135/220 (61%), Strand = Minus / Plus

Query:    237 TTTTTTTTTTTTGCCACGTAGAATTT-TATTGATCTGACTACTAGTTTGACAATTTAAT-T 180
                T TT TTT T G C C  A AAT T TATT  TC  ACTACTAGTTTG  AA   AAT T
Sbjct:   3342 TATTGTTTGTCGTCTCAGAAAAATATGTATTTTTCC-ACTACTAGTTTGCAAAGAAAATAT 3400

Query:    179 CACATAGTA-AAGTCCTTTGGGTAAACTTCATGACGAACT-CTTTCACAGTACTCCAATA 122
                A  TAGTA AA T  TTTG  A ACTTCAT A A CT C TTCA A T CT    TA
Sbjct:   3401 GATTTAGTATAAATT-TTTGAC-ATACTTCATAAAAATCTGCATTCA-ATTCCTGAGGTA 3457

Query:    121 A-CTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCC-G-AATGGATAATAGA 65
                 C TT    G   TTT G AA     GAAA  T ATT  G G AA  GATAATA
Sbjct:   3458 TTCCTTTATTCGGATGTTT-GT-AATTGGTGAAAGTTTATTTTGTGTAAAAGATAATA-- 3513

Query:     64 CAGTTGCCAATTGAGAG--AAGACTGTTGCATCCGCCGC-CGTGATTTCC 18
                C GT G  AT GAGA  AA AC GT G AT  GC GC C TGATTT C
Sbjct:   3514 C-GT-GAAGAT-GAGAATAAAAACAGTAGGATA-GCGGCTCCTGATTTTC 3559



>Y71G12B [Full Sequence]  [AceBrowser]   ACC=AC025726
        Length = 191,954


   Plus Strand HSPs:


   Score = 143 (21.5 bits), Expect = 0.50, Sum P(2) = 0.39
   Identities = 117/199 (58%), Positives = 117/199 (58%), Strand = Plus / Plus

Query:     43 GTCTTCTCTCAATTGGCAA-CTGTCTATTATCCATTCCGCAATCACATT--TC-GGATGT 98
```

```
                    GT TTCT T AA T  CAA CTG   ATT TCCATT     AAT A A    T  GG TG
Sbjct:  125097 GTTTTCTGTGAAATTTCAAGCTGAA-ATT-TCCATTTTTGAATAAAAAAAATGTGGCTGG 125154

Query:      99 -TCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGA-GTTCGTCA-TGAAGT 155
                    T T  AAAA  AC    AAA T ATT    ACTG AAA    GT   TC  TGAA T
Sbjct:  125155 ATTTAAAAAAAAACCATTAAAAATTGATTTTTTAACTGAAAAATCCGTATTTCTCTGAAAT 125214

Query:     156 TT-ACCCAAAGGACTTTACTATGTGAA-TTAAATTGTCAAACTAGTAGTCAGATCAATAA 213
                   TT A  CAAA  A  T A T T  GAA TTAAA   T  AC A  A TCA AT AA
Sbjct:  125215 TTCAGGCAAAAAATGTCATT-TCCGAAATTAAAAATTGCGACAAA-A-TCAAATAAAATT 125271

Query:     214 AATTCTACGTGGCAAAAAAAAAAAA 238
                   AT C A  T GCAAAAAAAAAAAA
Sbjct:  125272 GAT-CAAATTTGCAAAAAAAAAAAA 125295
```

 Score = 107 (16.1 bits), Expect = 0.50, Sum P(2) = 0.39
 Identities = 33/46 (71%), Positives = 33/46 (71%), Strand = Plus / Plus

```
Query:       1 TTTTTTTTTTTTTGGGAGGAAATCACGGCGGCGGATG-CAACAGTC 45
                   TTTTTTTTTTTTTG GA   A TCAC  CG CG AT   CAA A TC
Sbjct:   56244 TTTTTTTTTTTTTTGAGAAATATTCACAACGTCGCATTACAAAATTC 56289
```

>Y49F6A [Full Sequence]  [AceBrowser]   ACC=AC024800
       Length = 24,330

  Plus Strand HSPs:

 Score = 153 (23.0 bits), Expect = 0.77, P = 0.53
 Identities = 67/99 (67%), Positives = 67/99 (67%), Strand = Plus / Plus

```
Query:     140 GAGT-TCGTCATGAAGTTTACCCAAAGGACTTTACTATGTGAATTAAATTGTCAAA-CTA 197
                   GAGT T G AT AA TTTACC  AA  A T C  A T AA  AAA T  CAAA CTA
Sbjct:   18916 GAGTATTGCAAT-AATTTTACCTTAAA-ATTGTTCAAA-TAAAAAAAAAATAACAAAACTA 18972

Query:     198 GTAGTCAGATCA-ATAAAATTCTACGTGGCAAAAAAAAAAAA 238
                   GTAGTCA A CA A  AAAATT   CGTG  AAAA  A AAAA
Sbjct:   18973 GTAGTCAAACCAGACAAAATTGC-CGTGAAAAAAGCAGAAAA 19013
```

>F54B3 [Full Sequence]  [AceBrowser]   ACC=Z48583
       Length = 33,200

  Plus Strand HSPs:

 Score = 152 (22.8 bits), Expect = 0.85, P = 0.57
 Identities = 118/186 (63%), Positives = 118/186 (63%), Strand = Plus / Plus

```
Query:      49 TCTCAATTGGCAACTGTCT-ATTATCCATTCCGCAATCACATT--TCGGATGTTCTCGAA 105
                   TCTCAAT  G AA TG CT AT ATC AT   GCAAT A TT  TCG A T T   A
Sbjct:   25833 TCTCAAT--G-AA-TGGCTGATAATCTATGT-GCAATGATTTTGATCGAAAATG-TATTA 25886

Query:     106 AAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGA--GT-TCGTC-ATGAAGTTTACCC 161
                   AA ACTTCCCA  TT T  GA ACT  A A   GT T  TC AT AA TTTACC
Sbjct:   25887 AAT-ACTTCCCACT-TT-TCAGAAAACTAACAGATTCCGTGTATTCTATAAA-TTTACCT 25942

Query:     162 AAAGGACTTTACTATGTGAA-TTAAATTGTCAAACTAGTAGTCAGATC-AAT-AAAATTC 218
                   AA A TT A T T TG A TT A   TCAA T GTA  C   TC AAT AAAATTC
Sbjct:   25943 CAACTAATTCAATTTTTGTAGTTCTACC-TCAATATTGTACCCGCCTCCAATCAAAATTC 26001
```

```
Query:   219 TACGTGGCAAAAAAAA 234
             TACGT   AA AAAAA
Sbjct: 26002 TACGTCAGAATAAAAA 26017
```

Minus Strand HSPs:

Score = 142 (21.3 bits), Expect = 2.4, P = 0.91
Identities = 88/141 (62%), Positives = 88/141 (62%), Strand = Minus / Plus

```
Query:   234 TTTTTTTTGCCACGTAGAATTTTATTGATC-TGACTACTAGTTTGACAATTTAATTCACA 176
             TTTTTTTTGCC C A AATTT A T AT T  TA T GTT GA   TTTAA  C CA
Sbjct: 11113 TTTTTTTTGCCCCAAAAAATTTCAATTATAATTTTTATTTGTTGGATTTTTTAACACCCA 11172

Query:   175 TA-GTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACTCCAATAACTTT 117
              A G AAA   TT G T    TT  T A AA T TTTC CA TA T CAA AA TTT
Sbjct: 11173 AAAGCAAAAAATTTACGTTTTTTTTTCT-AT-AA-T-TTTCCCAATAATTCAA-AA-TTT 11226

Query:   116 GGG-A-AGTCC-TTTTCGAGAACATC 94
             G G A  C  TTTTC  GAACA C
Sbjct: 11227 GTGTACAAACAATTTTCAGGAACAAC 11252
```

>C03A7 [Full Sequence]  [AceBrowser]  ACC=AF016451
       Length = 41,609

Plus Strand HSPs:

Score = 152 (22.8 bits), Expect = 0.85, P = 0.57
Identities = 92/139 (66%), Positives = 92/139 (66%), Strand = Plus / Plus

```
Query:    95 ATGTTCTCGAAAAGGACTTCCCA-AAGTTATTGGAGTACTGTGAAAGAGT-TCGTCAT-G 151
             ATGTT T G AA GG  TT C A AAG A TG   T T TGAAA AGT T G CAT G
Sbjct: 11864 ATGTTATTGTAA-GG--TTACTAGAAGGAAGTGTTTTTTTTTGAAAAAGTATAGACATTG 11920

Query:   152 AAGTTTACCCAAAGGA--CTTTACTATGTGAATTAAA-TTGTCAAACTAGTAGTCAGATC 208
             A GT T C CAA G    CTTTA TAT T AATTAAA TTGT    C  TG AG T
Sbjct: 11921 ACGTCT-CTCAATGTTTTCTTTAATAT-T-AATTAAAAATTGTTTTTCATTTTGAAAGTTT 11977

Query:   209 --AA-TAAAATT-CTACGTGGCAAA 229
               AA T AAATT CTACGTGGCAAA
Sbjct: 11978 TAAAATCAAATTTCTACGTGGCAAA 12002
```

>ZK287 [Full Sequence]  [AceBrowser]  ACC=Z70757
       Length = 39,874

Minus Strand HSPs:

Score = 149 (22.4 bits), Expect = 1.2, P = 0.69
Identities = 135/234 (57%), Positives = 135/234 (57%), Strand = Minus / Plus

```
Query:   234 TTTTTTTTGCCACG-TAGAATTTTATTGATCTGACTACTAGTTTGACAATTTAATTCACA 176
             T TTTT T C AC  T GA TTTT TTG T   CTACT TT  CA  T  TCACA
Sbjct: 20947 TATTTTATACTACCCTTGATTTTT-TTG-TAAACCTACTTCTTAAGCAGAGTCTCTCACA 21004

Query:   175 TAGTAAAGTCCTTTGGGTA-AACTTCATGACGAACTCT-T-TC-ACAGTACTCCAATAAC 120
                 T  GT CTTT   TA AAC T AT A  A  TC  T TC AC G A T  AA AAC
Sbjct: 21005 CT-T---GTTCTTTTTATAGAACCT-ATTATCATTTCCATCTCTACCGGAATAGAAGAAC 21059
```

5/17/01 12:16 PM

```
Query:    119 TTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCGGAATGGATAATAGACAGTT 60
              T    A T CTT   GA    ATC GAAAT   AT G GGAAT     AAT G C GTT
Sbjct:  21060 CGTTCACATTTCTTAGTGACTCGATC-GAAATAATATCGAGGAATATTGAATGGCCCGTT 21118

Query:     59 GCCAATTGAGAGAAGACTGTTGCATCCGCCGCCGTGATT--TCCTCCCAAAAAAAAAAAAA 2
              GCCAATTG   G  GA  GTT CA  CG      TG TT  T TCC AAAAAA  AAA
Sbjct:  21119 GCCAATTGCTGGTGGAA-GTT-CACACGATTTTCTGGTTGGTTTTCCTAAAAAATTAAAT 21176

Query:      1 A 1
              A
Sbjct:  21177 A 21177
```

>Y22D7AL [Full Sequence]    [AceBrowser]    ACC=AC084153
          Length = 89,370

  Minus Strand HSPs:

 Score = 147 (22.1 bits), Expect = 1.4, P = 0.76
 Identities = 99/156 (63%), Positives = 99/156 (63%), Strand = Minus / Plus

```
Query:    238 TTTTTTTTTTTTGCCACGTAGAATTTTATTGATCTGACTACTAGTTTGACAATTTAATTC 179
              TTTTTTTTTTTT    A GT  AATTTT TT  TCTGA T  T   TT GA AATT  AA
Sbjct:  53522 TTTTTTTTTTTTTTAAATGTCAAATTTTTTT--TCTGAATTTT--TTCGAAAATTAAAAAA 53577

Query:    178 ACATAGTAAAG-TCC-TT-TGG-GTAAACTTCATGACGAACTCTTTC-ACAGTACTCCAA 124
              C T   TAAA  TC  TT T    GTAAA    ATG CG A T T   A ATA T  AA
Sbjct:  53578 TCCTCCTAAAAATCAATTATTCAGTAAAAA--ATGTCGGAATTTATATATA-TA-TGGAA 53633

Query:    123 TAACTTTGGGAAGTCCTTTTCGAGAACATCC-GAAATGTGAT 83
              AA TT   GA  T   TTTTCG GAA A CC GAAA G GAT
Sbjct:  53634 GAAATTATTGATTT--TTTTCGGGAAAAACCTGAAAAGCGAT 53673
```

>Y11D7A [Full Sequence]    [AceBrowser]    ACC=AL032632
          Length = 57,337

  Plus Strand HSPs:

 Score = 146 (21.9 bits), Expect = 1.6, P = 0.80
 Identities = 112/181 (61%), Positives = 112/181 (61%), Strand = Plus / Plus

```
Query:     45 CTTCTCTCAATTGGCAACTGTCTATTATCC-ATTCCGC--AA-TCACATTTCGGATGTTC 100
              CTTCT TCAA  G CAACTGTCTAT AT C ATT   C  AA T A TTTCG  TGTT
Sbjct:   4520 CTTCT-TCAACCGCCAACTGTCTATAATTCGATTTGTCTTAAATTAT-TTTCGACTGTT- 4576

Query:    101 TCGAAAAGGACTTCCCAA-AG-T-TATTGGAGTACTGTGAA-AGA-GTTCGTCATG-A-A 153
              TC A A G   C T    AA AG T TATTGGA T  TG  AA A A G TC TC TG A A
Sbjct:   4577 TCAAGATGTTCATATAAACAGATCTATTGGAATTTTGACAACAAACGCTC-TC-TGTATA 4634

Query:    154 GTTTACCCAAAGGACTTTACTAT-GTGAATTAAATTGTCAAACTAGTAGTCAGATCA-AT 211
              TTTA  A  A  TT C AT GT  TTAA TT   AAA   G A  CA A CA AT
Sbjct:   4635 TTTTAGAAAGATTAAATTCCAATAGTTC-TTAATTTAAAAAAAACGAATGCAAAACACAT 4693

Query:    212 AAAATTC 218
              A  TTC
Sbjct:   4694 GATTTTC 4700
```

>C46B10 [Full Sequence]   [AceBrowser]    ACC=AF039710
          Length = 30,237

   Plus Strand HSPs:

   Score = 145 (21.8 bits), Expect = 1.8, P = 0.83
   Identities = 55/79 (69%), Positives = 55/79 (69%), Strand = Plus / Plus

Query:     38 CAACAGTCTTCTCTCAATTGGCAACTGTC-TATTATCCATTCCGCAATCACATTTCGGAT 96
              CAAC G  TT TCTCAATTGGCA  TGTC TATT T CATT  CA  C CA T CGG T
Sbjct:  14038 CAAC-GCGTTTTCTCAATTGGCACTTGTCGTATT-TGCATTTA-CACACTCAGT-CGGTT 14093

Query:     97 GTTCTCGAAAAGGACTTCCC 116
              TC C AA AG ACTTC C
Sbjct:  14094 TCTCACAAACAGTACTTCGC 14113




>F23H11 [Full Sequence]   [AceBrowser]    ACC=AF003389
          Length = 30,510

   Plus Strand HSPs:

   Score = 144 (21.6 bits), Expect = 2.0, P = 0.86
   Identities = 76/118 (64%), Positives = 76/118 (64%), Strand = Plus / Plus

Query:     47 TCTCTCAA-TTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGA-TGTTCTCGA 104
              TC CTCAA TTGGCAA  G C A  AT  T CCGCAA  C TTT  A TGTTC  GA
Sbjct:   1371 TCACTCAAATTGGCAA--G-C-AGCATGGCT-CCGCAAAG-C-TTTGAAAGTGTTCGTGA 1423

Query:    105 AAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAA 164
              AA GA TTCCCAAAGTTA     TACT T A GA   T ATG  GTTTAC CAAA
Sbjct:   1424 CAAAGAATTCCCAAAGTTAAAATGTTACTTTTCATGAAAAAATAATGT-GTTACTCAAA 1482




>T24C4 [Full Sequence]   [AceBrowser]    ACC=AF100306
          Length = 31,917

   Plus Strand HSPs:

   Score = 144 (21.6 bits), Expect = 2.0, P = 0.86
   Identities = 76/118 (64%), Positives = 76/118 (64%), Strand = Plus / Plus

Query:     47 TCTCTCAA-TTGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGA-TGTTCTCGA 104
              TC CTCAA TTGGCAA  G C A  AT  T CCGCAA  C TTT  A TGTTC  GA
Sbjct:  31288 TCACTCAAATTGGCAA--G-C-AGCATGGCT-CCGCAAAG-C-TTTGAAAGTGTTCGTGA 31340

Query:    105 AAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAA 164
              AA GA TTCCCAAAGTTA     TACT T A GA   T ATG  GTTTAC CAAA
Sbjct:  31341 CAAAGAATTCCCAAAGTTAAAATGTTACTTTTCATGAAAAAATAATGT-GTTACTCAAA 31399




>Y53H1A [Full Sequence]   [AceBrowser]    ACC=AL132864
          Length = 27,963

   Minus Strand HSPs:

```
Score = 143 (21.5 bits), Expect = 2.2, P = 0.89
Identities = 71/117 (60%), Positives = 71/117 (60%), Strand = Minus / Plus

Query:   235 TTTTTTTTTGCCACGTA-GAATTTTATTGATCTGACTACTAGTTTGACAATTTAATTCAC 177
             TTTTTTTTTGC A   A G  TTTT TT AT TGA T  TAGTTT ACAATTT      A
Sbjct: 10404 TTTTTTTTTGCAAAAAAAGGCTTTTTTT-ATTTGAATTTTAGTTTTACAATTTTCGAGAA 10462

Query:   176 ATAGTAAAGTC-CTTTGGGTAAACTTCATGA-CGAACTCTTTCACAGTACTCCAATAA 121
             AT G AAA TC C TT   T A TT T A CGAA   TT A T T A TAA
Sbjct: 10463 ATTGAAAATTCACATTTTATGGAATTTTTAATCGAAAAAATTGAAATTTTTAAACTAA 10520



>T07C12 [Full Sequence]   [AceBrowser]   ACC=Z73976
         Length = 33,482

   Minus Strand HSPs:


   Score = 143 (21.5 bits), Expect = 2.2, P = 0.89
   Identities = 105/176 (59%), Positives = 105/176 (59%), Strand = Minus / Plus

Query:   238 TTTTTTTTTTTTGCCACGTAGAATTTTATTGATCTGACTACTAGTTTGACAAT-TTAATT 180
             TTT  TTTTT T CC C T GA  TT    T  G C  T   TTG   T TT ATT
Sbjct: 30677 TTTAGTTTTTCTCCCTCATTGACCTCTCGAAGTGAGCCGTTTCCGTTGTGTTTGTTGATT 30736

Query:   179 CACATAGTAAAGTCCTTTGGGTAAACTTCAT-GA--CGAACTCTTTCACAGTACTCCAAT 123
             CA A TAA GTCC T   T  CTTCA GA  CGAACTCTTTC C GT    AA
Sbjct: 30737 ATCA-ACTAAGGTCCGTATCTTC--CTTCAGAGATGCGAACTCTTTCGCCGTGAGATAAG 30793

Query:   122 AACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGCG-GAATGGATAATAGAC 64
             ACTTT G AAG C TTTTC AGA  AT G  ATGTG TT  G GAA G A AA A AC
Sbjct: 30794 CACTTTCGAAAGAC-TTTTCTAGAGGATAAGTGATGTG-TTAAGAGAA-G-A-AACAAAC 30848

Query:    63 A 63
             A
Sbjct: 30849 A 30849



>B0285 [Full Sequence]   [AceBrowser]   ACC=Z34533
         Length = 41,397

   Minus Strand HSPs:

   Score = 143 (21.5 bits), Expect = 2.2, P = 0.89
   Identities = 121/201 (60%), Positives = 121/201 (60%), Strand = Minus / Plus

Query:   237 TTTTTTTTTTTTGCCACGTAGAATTTTATTGA-TCTGACTACT-AGTTTGACAATTTAAT- 181
             TT TTT  T TGC AC TAGAA   AT GA T GA  A T A TTT   AA T AAT
Sbjct: 11406 TTGTTTCCTCTGC-AC-TAGAAGGCGATGGACTAGGATCAGTGACTTTCTGAAAT-AATG 11462

Query:   180 TCACATAGTAAAGTCCTTTGG-GTAAACTTCATGACGAA--CTCTTTCACAGT-ACTCCA 125
             T A AT    A A TC TT   G AA T ATG   AA  CTCT T A G  ACTCCA
Sbjct: 11463 TTAAATTTCAGAATCTTTAAATGGAGAATAAATGTTAAAACCTCTGTAATCGCGACTCCA 11522

Query:   124 ATAA-CTT-TGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTGC----GGAATGGAT 71
             TA CTT T  G A TCCTTTTCGAG CATCC A  T ATT C   GGAA GGAT
Sbjct: 11523 -TATTCTTGTTCGTATTCCTTTTCGAGCGCATCCCACGGATTATTCCACATGGAAGGGAT 11581

Query:    70 AATAGACA-GTT-GC--CAATTGAG 50
             ATA A  GTT GC  CAATTG G
```

```
Sbjct: 11582 TATACATTTGTTCGCGTCAATTGGC 11606
```

>F10G2 [Full Sequence]   [AceBrowser]   ACC=U64836
      Length = 26,539

  Plus Strand HSPs:

 Score = 142 (21.3 bits), Expect = 2.4, P = 0.91
 Identities = 90/144 (62%), Positives = 90/144 (62%), Strand = Plus / Plus

```
Query:    81 CAATCACATTTCGGATGTTCT-CGAAAAGGACTTCCCAAAGTTATTGGAG-TACTGTGAA 138
             CA TC CA  C ATGTTC  C AAA  AC TCC AA     TT G G T C G GAA
Sbjct: 8787 CATTCCCAAA-CAAATGTTCCACTGAAAT-ACGTCCAAATACGGTTAGTGCTCCAG-GAA 8843

Query:   139 A-GAGTTCGTCATGAAGTTTACCCAAAGGACTTT-ACTATGTGAAT-TAAATTGTCAAAC 195
             GA     TCATGA G TTA   AAAGGA   T A TA   T AA   T A TT T AAA
Sbjct: 8844 CTGAAAAA-TCATGAGGCTTAAAAAAAGGAAAATCATTAGATCAACCTCAGTT-TGAAAG 8901

Query:   196 TAGTAGTCAGATCAATAAAATTCTACGTG 224
             TA  AGTCA ATCAATAAAAT  TA GTG
Sbjct: 8902 TAAAAGTCATATCAATAAAATA-TA-GTG 8928
```

>Y48G1A [Full Sequence]   [AceBrowser]   ACC=AC024792
       Length = 43,096

  Plus Strand HSPs:

 Score = 142 (21.3 bits), Expect = 2.4, P = 0.91
 Identities = 70/119 (58%), Positives = 70/119 (58%), Strand = Plus / Plus

```
Query:   116 CAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGACTTTACTA 175
             CA GT A TGGA TA  G GAA G GT CG C  GA GTT A    AAG A    A  A
Sbjct: 16256 CAGGGTGAATGGAATAAGGAGAA-GCGTACGGCG-GATGTTGAGAAGAAGAAGGACAAGA 16313

Query:   176 TGTGAATTAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGGCAAAAAAAA 234
              T A TTAAATT TC A T  T GT  G T AA A A T TA TGGCAAAAAAAA
Sbjct: 16314 AATAATTTAAATTTTCCTATTTTTTGTTTGTTGAAAATGACTTTATTTGGCAAAAAAAA 16372
```

>F56G4 [Full Sequence]   [AceBrowser]   ACC=Z81552
      Length = 38,062

  Minus Strand HSPs:

 Score = 141 (21.2 bits), Expect = 2.7, P = 0.93
 Identities = 99/158 (62%), Positives = 99/158 (62%), Strand = Minus / Plus

```
Query:   238 TTTTTTTTTTTTGCCACGTAGAATTTTATTGATCTGA-CTACTAGTTTGA-CAATTTAAT 181
             TTT T  TTTT  AC AGAATTTTATTGAT T  CTAC AGTTT A C ATTT  T
Sbjct: 20506 TTTATCGATTTTTTAAC--AGAATTTTATTGATTTTTTCTAC-AGTTTATCGATTTT-T 20561

Query:   180 TCACATAGTAA-AGTCCTTTGGG-TAAACTTCATGACGAACTCTTTCACAGTACTCCAAT 123
             T ACA A T  A T  TTT    TA TT T CGA T TTT ACAG A T  A T
Sbjct: 20562 TAACAGAATTTTATTGATTTTTTCTACAGTTT-TATCGATTT-TTTAACAGAATTTTATT 20619

Query:   122 AACTTTGGG-A-AGTCCTTTTCGAGAAC-ATCCGAAATGTGATTG 81
```

```
                   A TTT    A AGT  TT TCGA      A CCGAA  T T ATTG
Sbjct: 20620 GATTTTTTCTACAGTT-TTATCGATTTTTAACCGAATTTT-ATTG 20662

  Score = 141 (21.2 bits), Expect = 2.7, P = 0.93
  Identities = 99/158 (62%), Positives = 99/158 (62%), Strand = Minus / Plus

Query:    238 TTTTTTTTTTTTTGCCACGTAGAATTTTATTGATCTGA-CTACTAGTTTGA-CAATTTAAT 181
               TTT T   TTTT   AC  AGAATTTTATTGAT T   CTAC AGTTT A C ATTT  T
Sbjct: 20720 TTTATCAATTTTTTAAC--AGAATTTTATTGATTTTTTCTAC-AGTTTTATCGATTTT-T 20775

Query:    180 TCACATAGTAA-AGTCCTTTGGG-TAAACTTCATGACGAACTCTTTCACAGTACTCCAAT 123
               T ACA A T   A T TTT    TA ATT  T CGA  T TTT ACAG A T  A T
Sbjct: 20776 TAACAGAATTTTATTGATTTTTTCTACAGTTT-TATCGATTT-TTTAACAGAATTTTATT 20833

Query:    122 AACTTTGGG-A-AGTCCTTTTCGAGAAC-ATCCGAAATGTGATTG 81
                A TTT    A AGT  TT TCGA      A CCGAA T T ATTG
Sbjct: 20834 GATTTTTTCTACAGTT-TTATCGATTTTTAACCGAATTTT-ATTG 20876

  Score = 141 (21.2 bits), Expect = 2.7, P = 0.93
  Identities = 99/158 (62%), Positives = 99/158 (62%), Strand = Minus / Plus

Query:    238 TTTTTTTTTTTTTGCCACGTAGAATTTTATTGATCTGA-CTACTAGTTTGA-CAATTTAAT 181
               TTT T   TTTT   AC  AGAATTTTATTGAT T   CTAC AGTTT A C ATTT  T
Sbjct: 21063 TTTATCGATTTTTTAAC--AGAATTTTATTGATTTTTTCTAC-AGTTTTATCGATTTT-T 21118

Query:    180 TCACATAGTAA-AGTCCTTTGGG-TAAACTTCATGACGAACTCTTTCACAGTACTCCAAT 123
               T ACA A T  A T TTT    TA A TT T CGA  T TTT ACAG A  A T
Sbjct: 21119 TAACAGAATTTTATTGATTTTTTCTACAGTTT-TATCGATTT-TTTAACAGAATTTTATT 21176

Query:    122 AACTTTGGG-A-AGTCCTTTTCGAGAAC-ATCCGAAATGTGATTG 81
                A TTT    A AGT  TT TCGA      A CCGAA T T ATTG
Sbjct: 21177 GATTTTTTCTACAGTT-TTATCGATTTTTAACCGAATTTT-ATTG 21219

  Score = 138 (20.7 bits), Expect = 3.7, P = 0.97
  Identities = 78/122 (63%), Positives = 78/122 (63%), Strand = Minus / Plus

Query:    238 TTTTTTTTTTTTTGCCACGTAGAATTTTATTGATCTGA-CTACTAGTTTGA-CAATTTAAT 181
               TTT T   TTTT   AC  AGAATTTTATTGAT T   CTAC AGTTT A CAATTT  T
Sbjct: 20677 TTTATCGATTTTTTAAC--AGAATTTTATTGATTTTTTCTAC-AGTTTATCAATTTT-T 20732

Query:    180 TCACATAGTAA-AGTCCTTTGGG-TAAACTTCATGACGAACTCTTTCACAGTACTCCAAT 123
               T ACA A T  A T TTT    TA A TT T CGA  T TTT ACAG A  A T
Sbjct: 20733 TAACAGAATTTTATTGATTTTTTCTACAGTTT-TATCGATTT-TTTAACAGAATTTTATT 20790

Query:    122 AACTTT 117
               A TTT
Sbjct: 20791 GATTTT 20796




>W03B1 [Full Sequence]  [AceBrowser]   ACC=U58753
       Length = 38,152

  Plus Strand HSPs:

  Score = 141 (21.2 bits), Expect = 2.7, P = 0.93
  Identities = 131/223 (58%), Positives = 131/223 (58%), Strand = Plus / Plus

Query:      1 TTTTTTTTTTTTTGGGAGGAAATCA-CGG----CGGCGGATGCAACAGTCTTCTCTCAAT 55
               T TTTTTTTTTT GGA  AAATCA C      CG C GA GC A AGTC     A T
Sbjct: 18749 TGTTTTTTTTTTTTGGAAAAAAATCAACATTTTTCGACCGAAGCCA-AGTCAAGAAA-ATT 18806
```

```
Query:    56 TGGCAACTGTCTATTATCCATTCCGCAATCACATTTCGGATGTTCTCGAAAAGGACTTCC 115
             TG AACT T ATT T        AATCA ATTT   T T  CG A   A TTCC
Sbjct: 18807 TGAAAACTTTAGATTTTTTCCAAAAAAATCAAATTTACC-TCTAAACGTTATATA-TTCC 18864

Query:   116 CAAAGTTATTGGAGTACT-GTGAAAGAGTTCG-TCATGAAGTTT-ACCCAAAGGACTTTA 172
                AGT T G AG ACT GTGAAA A T C  T A G A TTT A CCAAAG A T  A
Sbjct: 18865 TCGAGTCCTCG-AG-ACTAGTGAAAAAATGCACTGAAGCAATTTCAGCCAAAGTA-TGAA 18921

Query:   173 CTATG-TGAATTAAATTGTCAAACTAGTAGTCAG-ATC-AATAAAATTCTA 220
             C ATG T A  AT T   AC AGT GT A  ATC AATAA AT C A
Sbjct: 18922 C-ATGATCTACCCATTCTTTGCACAAGTTGTAAACATCTAATAATATGCGA 18971
```

>Y48A6B [Full Sequence]   [AceBrowser]    ACC=AL023844
              Length = 75,073

   Plus Strand HSPs:

 Score = 141 (21.2 bits), Expect = 2.7, P = 0.93
 Identities = 79/117 (67%), Positives = 79/117 (67%), Strand = Plus / Plus

```
Query:   116 CAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACC-CAAAGGACTTTACT 174
             CAA GTT TT A T T AAA AGTT   AT AGTT A C A GGA TTT CT
Sbjct:  8650 CAAGGTT-TTATAATT-TAT-AAA-AGTTAA--ATACAGTTAAACACTAGGGATTTTGCT 8703

Query:   175 --ATGTGA-ATTAAATTGTCAAACTAGT-AG-TCAGATCAATAAAATTCTACGTGGCAAA 229
               A TGA A  AAAT G  AAACTA  A  T AGAT AATAAAATTCT CG G  AAA
Sbjct:  8704 TGAAATGATAGAAAATAGA-AAACTAAACATATAAGATTAATAAAATTCTTCGAGAAAAA 8762

Query:   230 AAA 232
             AAA
Sbjct:  8763 AAA 8765
```

>T24C12 [Full Sequence]   [AceBrowser]    ACC=U41037
              Length = 18,633

   Plus Strand HSPs:

 Score = 140 (21.0 bits), Expect = 3.0, P = 0.95
 Identities = 92/150 (61%), Positives = 92/150 (61%), Strand = Plus / Plus

```
Query:    89 TTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTC 148
             TT CG A GTTCT GAA A A   CC AAA   AT G A T CTG GAAA   TT  T
Sbjct: 16285 TTGCGAAAGTTCTTGAAGATCAG--CCGAAAC--ATCGAA-TGCTG-GAAAATTTTTTTG 16338

Query:   149 ATGAAGTTTACCCAAAGGACTTTACTA--TG-TGAATTAAATTGTCAAACTAGTAGTCAG 205
             TG      A   AAAG ACTT A TA  TG T AA  AAATTGTC AA T    A
Sbjct: 16339 CTGTTCGGAAAAAAAGAACTTGAATAAATGGTAAAAAAAATTGTCCAAATTCAACAATT 16398

Query:   206 ATCAATAAAA-TTCTACGTGGCAAAAAAAAAAAAA 238
             TC  TAAAA TTC ACG G CAAAAAAAAAA A
Sbjct: 16399 TTCC-TAAAACTTC-ACGGGTCAAAAAAAAAAACA 16430
```

>F21D5 [Full Sequence]   [AceBrowser]    ACC=Z54271
              Length = 21,173

Minus Strand HSPs:

Score = 140 (21.0 bits), Expect = 3.0, P = 0.95
Identities = 76/122 (62%), Positives = 76/122 (62%), Strand = Minus / Plus

```
Query:    238 TTTTTTTTTTTTGCCACGTAGAATTTTATTGATCTGACTACT-AGT-TTGACAATTTAAT 181
              TTT   TTTTTTT C  CG AGAATTTTATT AT T  CTACT A T TT A  ATTT
Sbjct:   3089 TTTCCTTTTTTTTCTCCG-AGAATTTTATT-ATTTAGCTACTTAATATTTATTATTTGTC 3146

Query:    180 TCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACTCCAATAA 121
              TCA A GT   TCC TG T  CTT T  G CT TTTC C T T CAATAA
Sbjct:   3147 TCAAAACGTTTT-TCCAGTGATTTCTCTTTTTCT-GT-CT-TTTCTCTTTCTTGCAATAA 3202

Query:    120 CTTT 117
              TTT
Sbjct:   3203 TTTT 3206
```


>Y54E5A [Full Sequence]  [AceBrowser]    ACC=AL032643
          Length = 27,774

    Minus Strand HSPs:

 Score = 140 (21.0 bits), Expect = 3.0, P = 0.95
 Identities = 128/212 (60%), Positives = 128/212 (60%), Strand = Minus / Plus

```
Query:    238 TTTTTTTTTTTTGCCACGTA--GAATT-TTA--TTGA-TCTGACTA-CTAGTTTGACAAT 186
              TTTTTTTTT  TG A   A  GA TT TTA  TT  TC  A T  CTAG TT  CAA
Sbjct:  14778 TTTTTTTTTTCATGAAAAAGACGGATTTGTTAAATTTTGTCCAATTTTCTAGATTTTCAAG 14837

Query:    185 TTAATTCACATA-GTA-AAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACT 128
              T A TTCA A A GT  AAG C TT    TA CT A  ACGAACTCTTT A AG A T
Sbjct:  14838 TCATTTCA-AGACGTTCAAG-CGTTAAAATAG-CTCAAAAACGAACTCTTTGATAGCATT 14894

Query:    127 CCAATAACTT-TGGGAAGTCCTTTTCGAGAACA-TCC-GAAATGTGATT-GCGGAATGGA 72
              C  ATAA T T GA T C  TC AGAA  TC  GAA T G TT G  G AT A
Sbjct:  14895 CATATAAGTAGTCTGATTTGCAGATCCAGAATGCTCTTGAACTC-GTTTCGTCGTATC-A 14952

Query:     71 TAATAGACAGTTGCCAATTGAGAGAAGACTGTTGCA-TCC 33
              AA AG   TT CA TTGA A AAGA T T GCA TCC
Sbjct:  14953 CAA-AGTGTTTTATCAGTTGATACAAGA-TAT-GCAATCC 14989
```


>Y47D3A [Full Sequence]  [AceBrowser]    ACC=AL117202
          Length = 199,814

   Plus Strand HSPs:

 Score = 140 (21.0 bits), Expect = 3.0, P = 0.95
 Identities = 96/162 (59%), Positives = 96/162 (59%), Strand = Plus / Plus

```
Query:     83 ATCACATTTCGGATGTTCTCGAAAAGGACTTCCCAAAGTTATTGGAGTACTGTG-AAAGA 141
              A CA ATTTCG  T TT TC AAAA  ACT  C AAA TTA TG A T  T T AAA A
Sbjct: 155690 AGCATATTTCGACTATTTTCAAAAAAAACTCTCAAAAATTAGTGCATTTTTATTCAAAAA 155749

Query:    142 GTTCGTCATGAAG-TTTACCCAAAGGACTT-TA-CT--ATG-TGAATT-AAATTGTCAAA 194
                T G AT A TTTA  A G   TT TA CT A   TGA T  AAATTGTCAAA
Sbjct: 155750 AGTGGAAATTCACCTTTATATATTGATTTTCTATCTGAAAAATGACTGCAAATTGTCAAA 155809
```

```
Query:     195 CTAG-TAGTCAGATCAATAAAATTCTACG-TGG-CAAAAAAAA 234
                   AG TA    A ATCA  AAA TT  AC  T    CAA AAAAA
Sbjct: 155810 A-AGCTACGAAAATCACCAAATTTTGACTATTTTCAACAAAAA 155851
```

>ZK675 [Full Sequence]   [AceBrowser]    ACC=Z46812
      Length = 22,703

  Minus Strand HSPs:

  Score = 138 (20.7 bits), Expect = 3.6, P = 0.97
  Identities = 76/123 (61%), Positives = 76/123 (61%), Strand = Minus / Plus

```
Query:     141 TCTTTCACAGTACTCCAATAACTTTGG-GAAGTCCTTTTCGAGAACATCCGAA-ATG-TG 85
                   TC TTCAC G A  C AATAA TTTG  GAA TC  TTTCGAGAACAT   AA A   T
Sbjct:  15318 TCATTCACTGAAAACAAATAAATTTGTAGAA-TCTCTTTCGAGAACATGAAAATAAACTT 15376

Query:      84 ATTGCGGAATGGATAATAGACAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCCGCCGT 25
                   TT GGAA  GA AA A ACA  T     AT  A A A GA T T G AT CG  G   T
Sbjct:  15377 TTTGGGAAACGACAAAAAACATATATATATATATATA-GA-TATCG-ATACGGAGATTT 15433

Query:      24 GATTTC 19
                   GATT C
Sbjct:  15434 GATTCC 15439
```

>ZK1025 [Full Sequence]   [AceBrowser]    ACC=AL022288
      Length = 40,589

  Minus Strand HSPs:

  Score = 138 (20.7 bits), Expect = 3.7, P = 0.97
  Identities = 118/208 (56%), Positives = 118/208 (56%), Strand = Minus / Plus

```
Query:     209 TGATCTGACTACTAGTTTGACAATTTA-ATTC-ACATAGTAAAGTCCTTTGGGTAAACTT 152
                   TG TCTGA  A  A    TG CA TT A ATT  ACA AGT A T  TT     T A
Sbjct:     423 TGTTCTGATAAACACAATGTCACTTGATATTAGACAGAGTTTAATA-TTACTCTCACGAG 481

Query:     151 CATGACGAACTCT-TTCACAGTACTCCAATAACTTTGGGAA-GTCCTTTTCGAGAACATC 94
                   CA A  AACTC  TTCA A  T  ATA  TT G  A  G CC  T C    A ATC
Sbjct:     482 CAATAAAAACTCGGTTCAGAAAAGTAAACTATGTTCGAAATTGACCGGT-CATCCAGATC 540

Query:      93 CGAAATGTGATTG-CGGAATGGATAATAGACAGTTGCCA-ATTGAGAGAAGACTGTTGCA 36
                   CGAA T  G TT  CGG    G TA T  C  TTG  A ATTG  AG AGACT  T  A
Sbjct:     541 CGAACTTGGTTTTACGGCTCCGCTACTCT-CT-TTGAGACATTGTTAGGAGACTTCTCGA 598

Query:      35 TCCGCC-GCCGTGATTTCCTCCCAAAAAAAAAAA 4
                   CC C  G C    ATTTCC C CAAAAAAAAAA
Sbjct:     599 GCCACATGTCAC-ATTTCCACTCAAAAAAAAAAA 630
```

>D1065 [Full Sequence]   [AceBrowser]    ACC=AF016414
      Length = 21,095

  Minus Strand HSPs:

  Score = 137 (20.6 bits), Expect = 4.0, P = 0.98

Identities = 117/197 (59%), Positives = 117/197 (59%), Strand = Minus / Plus

```
Query:    237 TTTTTTTTTTTGCCA-CGTAGAATTTT-ATTGA-TCTGACTACTAGT-TTGACAATTTAA 182
              TT T TTTTT G A C   G ATTTT ATT   T TGA TA T GT TTGA A   T A
Sbjct:  10830 TTGTGTTTTTGGAGAGCACCGCATTTTTATTCTGTTTGA-TAATTGTATTGA-ATGTGAG 10887

Query:    181 TTCACATAGTAAAGTCCTTTGGGTAAACTTCATGACGAACTCTTTCACAGTACTCCAAT- 123
              T CA  AG A AT  T      AAACT ATGAC A  T T T ACAGTACTCCA
Sbjct:  10888 TACAACGAGAATAATTATGAAAACAAACTCAATGACTAGTTTTGTTACAGTACTCCAGCC 10947

Query:    122 AACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTGATTG-CGGAATGGATAATA-GA 65
              AACT   G   GC T TT G G A T C AAAT T AT G C GAAT GA A   A GA
Sbjct:  10948 AACTAATGTT-G-CATCTT-GTGTAAGTAC-AAATAT-ATCGTCAGAATAGAAACAACGA 11002

Query:     64 C-AGTTGCCAATTGAGAGAAGACTG 41
                AGT G AA T   GAA A TG
Sbjct:  11003 AGAGTGGG-AAGTCTCTGAAAATTG 11026
```

>LLC1 [Full Sequence]  [AceBrowser]  ACC=Z82277
   Length = 35,920

   Minus Strand HSPs:

 Score = 137 (20.6 bits), Expect = 4.1, P = 0.98
 Identities = 59/89 (66%), Positives = 59/89 (66%), Strand = Minus / Plus

```
Query:    178 ACATAGTAAAGTCCTTTGGGTAAACT-TC-AT-GACGAACTCTTTCACAGTACTCCAATA 122
              ACAT  T AAG  C T GG  AA T TC A  GAC A  T T TCA AG A  C  ATA
Sbjct:   8105 ACATCTTGAAGAGCATCGGA-AAGGTGTCCACCGACTAGAT-TCTCATAGCAACCGTATA 8162

Query:    121 ACTTTGGGAAGTCCTTTTCGAGAACATCCGA 91
              ACTTTG AA  CCTTTTCGAGAA A CCGA
Sbjct:   8163 ACTTTGCAAATGCCTTTTCGAGAAGAGCCGA 8193
```

>Y71F9AR [Full Sequence]  [AceBrowser]  ACC=AC024853
   Length = 50,768

   Minus Strand HSPs:

 Score = 137 (20.6 bits), Expect = 4.1, P = 0.98
 Identities = 93/149 (62%), Positives = 93/149 (62%), Strand = Minus / Plus

```
Query:    145 GAACTCTTTCACAGTACTCCAATAACTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGT 86
              GAACTCT   C T CTCC   A  TTT G A TC   T GAG A A CCGAAATG
Sbjct:  17864 GAACTCTGCGTCTCTTCTCCCGCATTTTTTGTAGATCTACGTAGAGCAAA-CCGAAATGA 17922

Query:     85 GA---T-TG-CGGAATGGATAATAG--ACAGTTGCCAA-TTGAGAGAAG-ACTGTTGCAT 35
              GA   T TG C  ATG  TAATAG A AGTTG  AA TT AGA AA  A T TTG AT
Sbjct:  17923 GACACTCTGACACCATGT-TAATAGGAAAAGTTGAAAAATTCAGAAAAACATTTTTGTAT 17981

Query:     34 CCGCCGCCGTGATTTCCTCCCAAAAAAAAAAAAAA 1
              GC T TTT T CCA AAAAAAAAAA
Sbjct:  17982 TAAATGCA-T--TTTGGTTCCACAAAAAAAAAAAA 18012
```

>Y53F4B [Full Sequence]  [AceBrowser]  ACC=AL132949

```
            Length = 227,206

    Plus Strand HSPs:

    Score = 137 (20.6 bits), Expect = 4.1, P = 0.98
    Identities = 79/131 (60%), Positives = 79/131 (60%), Strand = Plus / Plus

Query:      108 GGACTTCCCAAAGTTATTGGAGTACTGTGAAAGAGTTCGTCATGAAGTTTACCCAAAGGA 167
                G ACT  CCA   TT  T GA TA TG GA AGAGTTC TC  GAA TTT       G A
Sbjct:   177830 GAACTGGCCACT-TTCGTAGA-TAGTG-GACAGAGTTCTTCTGGAATTTTTTTTTTGGAA 177886

Query:      168 C--TTTACTATGTGAATTAAAATTGTCAAACTAGTAGTCAGATCAATAAAATTCTACGTGG 225
                    TTT  A  TGAA AAAATTG AA  TA  A T A A  AA AAAAT  TA G
Sbjct:   177887 AAATTTGAAAACTGAAA-AAATTGAAAATATATGAATAAAAAAAAAAAAATA-TATGAAT 177944

Query:      226 CAAAAAAAAAAAA 238
                AAAAAAAAAAAA
Sbjct:   177945 AAAAAAAAAAAAA 177957




>R10E11 [Full Sequence]   [AceBrowser]   ACC=Z29095
            Length = 32,458

    Plus Strand HSPs:

    Score = 136 (20.4 bits), Expect = 9.0, P = 1.0
    Identities = 54/78 (69%), Positives = 54/78 (69%), Strand = Plus / Plus

Query:      162 AAAGGACTTTACTATGTGAATTAAATTG-TCAAACTAGTAGTCAGATCAATAA-AATT-C 218
                A AGG  T T  TAT TGA TTA     G T AAACTA  A T A AT AA AA AATT C
Sbjct:    18780 ACAGGTATGTTTTAT-TGATTTATGAAGATAAAACTATAAATAA-ATGAAAAATAATTGC 18837

Query:      219 TACGTGGCAAAAAAAAAAAA 238
                TACGTGGCAA A AAAA AA
Sbjct:    18838 TACGTGGCAATACAAAACAA 18857




>F43C1 [Full Sequence]   [AceBrowser]   ACC=Z46937
            Length = 35,188

    Minus Strand HSPs:

    Score = 136 (20.4 bits), Expect = 9.0, P = 1.0
    Identities = 116/187 (62%), Positives = 116/187 (62%), Strand = Minus / Plus

Query:      216 ATTTTATTGATCTGACTAC-TAGTTTGACAATTTAATTCACA--TAGTAAAGTC-CTTTG 161
                ATTTTATT A T  TA  TA TT  A  TT ATTC C    T GT A G C CTT
Sbjct:     4126 ATTTTATTTAATTTATTAAATA-TTACAGTACTTGATTCCCTGGTCGTGATGCCTCTTCC 4184

Query:      160 GGTAAACTTCATGACGAACTCTTTCACAGTACTCCAATAACTTTGGGAAGTCCTTTTCGA 101
                    AAAC  C T AC AACTCTTTCAC  T  T CAAT ACTTT G AA TC T    C A
Sbjct:     4185 ACAAAC--C-T-ACAAACTCTTTCACTTTCTTTCAATCACTTTCGAAA-TC-TGC-C-A 4236

Query:      100 GAACATCCGAAATGTGATTGCG-GAATG-GATAATAGACAGTTGCCAATTGAGAGAAGAC 43
                GA   T GA AT GATTGC GAAT  GA A T   C G GC AAT  A A  AG C
Sbjct:     4237 GAT--TG-GATATCAGATTGCCCGAATTTGACATTTCTCCGA-GCAAATA-ATAATAGCC 4291

Query:       42 T-GTTGCATCCGCC 30
                T GT GCA C GCC
```

http:████w.sanger.ac.uk/cgi-bin/nph-Blast_Server.html

```
Sbjet:  4292 TTGTGCCA-CTGCC 4304
```

```
>C44H4 [Full Sequence]    [AceBrowser]    ACC=Z79598
         Length = 35,920
```

Minus Strand HSPs:

```
Score = 136 (20.4 bits), Expect = 9.0, P = 1.0
Identities = 116/200 (58%), Positives = 116/200 (58%), Strand = Minus / Plus
```

```
Query:   198 CTAGTTTGACAATTTAATTCACATAGTAAAGTC-CTTTGGGTAAACTTC--ATGACGAAC 142
               C A T T ACA  TTAA  CA  T  T A  T  C TT  GT A CTTC  ATG C AAC
Sbjct:  3929 CAATTGTTACAGATTAACGCAGTTGATGATTTTGCGTTCAGTCAGCTTCCTATG-CTAAC 3987
```

```
Query:   141 T-CT-TTCACAGTACTCCAATAA-CTTTGGGAAGTCCTTTTCGAGAACATCCGAAATGTG 85
               T CT TT A   AT A TAA C  T GAA TC TT  CGAG A AT   A AT  G
Sbjct:  3988 TTCTCTTGATTTGAGT--AGTAATCGATTAGAA-TCATTACCGAGCA-ATGTTATATACG 4043
```

```
Query:    84 ATTGCGGAATGGATAATAGACAGTTGCCAATTGAGAGAAGACTGTTGCATCCGCCGCC-G 26
               A T    ATG A AA A A  GT  CCA TT A AGAA ACT TT  AT C    G  G
Sbjct:  4044 ACTCATTGATGCAAAAGAAAACGTCACCAGTTCAAAGAAAACT-TTCAATTCAGAGTAAG 4102
```

```
Query:    25 TGAT-TTCCTCCCAAAAAAAAAAAAAA 1
               GA  TTC    CAAAAAAAAAAAA A
Sbjct:  4103 AGAAATTCAAAACAAAAAAAAAAAAGA 4128
```

Parameters:
  P=4
  warnings
  B=100
  V=100

  ctxfactor=2.00
  E=10

| Query Strand | MatID | Matrix name | ----- As Used ----- | | | ----- Computed ---- | | |
|---|---|---|---|---|---|---|---|---|
| | | | Lambda | K | H | Lambda | K | H |
| +1 | 0 | +5,-4 | 0.192 | 0.173 | 0.357 | same | same | same |
| | | q=10  r=10 | 0.104 | 0.0151 | 0.0600 | | | |
| -1 | 0 | +5,-4 | 0.192 | 0.173 | 0.357 | same | same | same |
| | | q=10  r=10 | 0.104 | 0.0151 | 0.0600 | | | |

| Query Strand | MatID | Length | Eff.Length | E | S | W | T | X | E2 | S2 |
|---|---|---|---|---|---|---|---|---|---|---|
| +1 | 0 | 238 | 238 | 10. | 136 | 11 | N/A | 73 | 0.023 | 74 |
| | | | | | | | | 79 | 0.025 | 100 |
| -1 | 0 | 238 | 238 | 10. | 136 | 11 | N/A | 73 | 0.023 | 74 |
| | | | | | | | | 79 | 0.025 | 100 |

Statistics:

  Database:  /data/blastdb/wormpub/allcmid
    Title:  wormpub/allcmid
    Release date:  unknown
    Posted date:  12:14 PM BST May 17, 2001
    Format:  BLAST
  # of letters in database:  104,258,147

```
# of sequences in database:  3692
# of database sequences satisfying E:   35
No. of states in DFA:   180 (360 KB)
Total size of DFA:  371 KB (384 KB)
Time to generate neighborhood:  0.01u 0.01s 0.03t  Elapsed: 00:00:00
No. of threads or processors used:  4
Search cpu time:  4.41u 1.80s 6.21t  Elapsed: 00:00:31
Total cpu time:  4.51u 1.83s 6.35t  Elapsed: 00:00:32
Start:  Thu May 17 17:10:32 2001   End:  Thu May 17 17:11:04 2001
```

script last modified Mon Apr 23 16:35:41 2001

webmaster@sanger.ac.uk

5/17/01 12:16 PM

| | | | | | | |
|---|---|---|---|---|---|---|
| T02G5.9 | CE04861 | lysyl-tRNA synthetase (ST.LOUIS) | +3 | 56 | 0.98 | 1 |
| T04C9.4B | CE26619 | (ST.LOUIS) | -1 | 48 | 0.98 | 1 |
| W10G11.16 | CE14830 | channel protein (ST.LOUIS) | -2 | 53 | 0.98 | 1 |
| K10D3.2 | CE25055 | locus:unc-14 (HINXTON) | -2 | 56 | 0.99 | 1 |
| F40G12.4 | CE10182 | (HINXTON) | -2 | 52 | 0.99 | 1 |
| F59E12.5 | CE11526 | (ST.LOUIS) | +3 | 54 | 0.996 | 1 |
| C08E3.8 | CE08011 | (ST.LOUIS) | -1 | 53 | 0.996 | 1 |
| F11G11.3 | CE07056 | Glutathione S-transferase (ST.LOUIS) | +1 | 55 | 0.998 | 1 |
| C46E10.9 | CE08767 | zinc finger protein (ST.LOUIS) | -1 | 52 | 0.999 | 1 |
| T04C9.4C | CE26620 | contains LIM-like binding domain ... | -1 | 48 | 0.9994 | 1 |
| Y22D7AR.3 | CE23432 | (ST.LOUIS) | +1 | 45 | 0.9996 | 1 |
| F52A8.1 | CE05908 | (HINXTON) | -2 | 46 | 0.9997 | 1 |
| ZK1037.6 | CE16758 | (HINXTON) | -2 | 52 | 0.9998 | 1 |

>F35E8.11 [Full Sequence] [AceBrowser] CE15961 Glutathione S-transferases. (HINXTON)
Length = 277

Plus Strand HSPs:

Score = 296 (104.2 bits), Expect = 9.2e-27, P = 9.2e-27
Identities = 56/58 (96%), Positives = 56/58 (96%), Frame = +1

Query:    4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177
             F F EEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM
Sbjct:  220 FLFGEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 277


>K01D12.12 [Full Sequence] [AceBrowser] CE06051 Glutathione S-transferases. (HINXTON
Length = 277

Plus Strand HSPs:

Score = 232 (81.7 bits), Expect = 5.6e-20, P = 5.6e-20
Identities = 42/58 (72%), Positives = 49/58 (84%), Frame = +1

Query:    4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177
             F F ++IT  DATVF QLA+VYYP R+HI+DVLEKDFPK+LEYCE VR EVYP DFT+
Sbjct:  220 FLFGDKITPTDATVFGQLASVYYPLRSHINDVLEKDFPKILEYCESVRKEVYPNDPTI 277


>K01D12.11 [Full Sequence] [AceBrowser] CE06050 Glutathione S-transferases. (HINXTOI
Length = 277

Plus Strand HSPs:

Score = 229 (80.6 bits), Expect = 1.2e-19, P = 1.2e-19
Identities = 41/58 (70%), Positives = 50/58 (86%), Frame = +1

Query:    4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177
             F F ++IT ADATVF QLATVYYP R+H++DVL+KDFPK+LEY ERVR E+YP DFT+
Sbjct:  220 FLFGDKITPADATVFGQLATVYYPIRSHLTDVLDKDFPKVLEYLERVRKEIYPNDFTI 277


>K01D12.13 [Full Sequence] [AceBrowser] CE06052 Glutathione S-transferases. (HINXTOI
Length = 287

Plus Strand HSPs:

```
Score - 216 (76.0 bits), Expect = 2.8e-18, P = 2.8e-18
Identities = 38/58 (65%), Positives = 45/58 (77%), Frame = +1

Query:     4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177
             + F + I   DATVFSQLA VYYPF  HIS VLE DFPK+L+YCER+R E+YP DFT+
Sbjct:   230 YLFGDHIAPVDATVFSQLAVVYYPFYTHISTVLENDFPKILQYCERIRKEIYPNDFTI 287




>C54D10.1 [Full Sequence]  [AceBrowser]  CE05497   Glutathione S-transferases. (HINXTON)
            Length = 278

  Plus Strand HSPs:

 Score = 215 (75.7 bits), Expect = 3.5e-18, P = 3.5e-18
 Identities = 38/58 (65%), Positives = 47/58 (81%), Frame = +1

Query:     4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177
             F F +++TAADA VF Q+A+V YPPR  I+D LE DFPK+LEYCERVR E+YP DFT+
Sbjct:   221 FLFGDKVTAADAAVFGQIASVIYPFRCSINDALENDFPKILEYCERVRQEIYPNDFTI 278




>C54D10.2 [Full Sequence]  [AceBrowser]  CE05498   Glutathione S-transferases. (HINXTON)
            Length = 315

  Plus Strand HSPs:

 Score = 213 (75.0 bits), Expect = 5.7e-18, P = 5.7e-18
 Identities = 39/56 (69%), Positives = 45/56 (80%), Frame = +1

Query:     4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDF 171
             F F +E+ AADA VF QLATV YPFR  I+D+LE DFP+LLEYCERVR E+YP DF
Sbjct:   258 FLFGDEVKAADAAVFGQLATVIYPFRCKINDILENDFPQLLEYCERVRKEIYPNDF 313




>K01D12.14 [Full Sequence]  [AceBrowser]  CE06053      (HINXTON)
            Length = 250

  Plus Strand HSPs:

 Score = 169 (59.5 bits), Expect = 2.6e-13, P = 2.6e-13
 Identities = 27/58 (46%), Positives = 43/58 (74%), Frame = +1

Query:     4 FFFWEEITAADATVFSQLATVYYPFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM 177
             + F ++IT+AD TVF ++A+ YYPF N S +++ +PKL EYC+R+  E+YP DF++
Sbjct:   193 YLFGDKITSADCTVFGEVASAYYPFPNKPSRIIDSHYPKLHEYCDRIIEELYPNDFSI 250




>C25H3.7 [Full Sequence]  [AceBrowser]  CE02505      (ST.LOUIS)
           Length = 275

  Plus Strand HSPs:

 Score = 153 (53.9 bits), Expect = 2.6e-11, P = 2.6e-11
 Identities = 26/55 (47%), Positives = 38/55 (69%), Frame = +1

Query:     4 FFFWEEITAADATVFSQLATVYY-PFRNHISDVLEKDFPKLLEYCERVRHEVYPK 165
             F F + IT+ D +VF Q+  V+Y P+R  ISD+LE DFP++  YC+R+R   YP+
```

```
Sbjct:   217 PLFGDRITSVDCSVFGQIGAVFYLPYRQQISDLLEDDFPRVRAYCDRIRQHYYPE 271
```

>Y48C3A.3 [Full Sequence]   [AceBrowser]  CE22138   (HINXTON)
        Length = 321

   Plus Strand HSPs:

  Score = 97 (34.1 bits), Expect = 6.4e-05, P = 6.4e-05
  Identities = 24/77 (31%), Positives = 41/77 (53%), Frame = +1

```
Query:     4 PFFWEEITAADATVFSQLATVYY-PFRNHISDVLEKDFPKLLEYCERVRHEVYPKDFTM* 180
             +F  + T DA +FS L  +YY P+ +   D+++ +   L EY ER+++  YP    +
Sbjct:   239 YFHGFKPTKVDACIFSHLCQIYYAPYTSEHRDLIDGECKNLAEYVERIKNRFYPDWDDVT 298

Query:   181 IKLSN**SDQ*NSTWQKK 234
             K S  +D  S W+K+
Sbjct:   299 TKFS---TD--TSNWKKR 311
```

>Y47H10A.1 [Full Sequence]   [AceBrowser]  CE24374   (HINXTON)
        Length = 638

   Plus Strand HSPs:

  Score = 61 (21.5 bits), Expect = 0.0058, Sum P(2) = 0.0058
  Identities = 11/44 (25%), Positives = 23/44 (52%), Frame = +2

```
Query:    98 FSKRTSQSYWSTVKEFVMKFTQRTLLCELNCQTSSQINKILRGK 229
             F +    +W ++K+F+++FT    C L+ T ++ K+  K
Sbjct:   419 FRIKEDGEFWMSLKDFMVEFTD-VYCCNLSADTMHEVEKMTEVK 461
```

  Score = 43 (15.1 bits), Expect = 0.0058, Sum P(2) = 0.0058
  Identities = 10/17 (58%), Positives = 11/17 (64%), Frame = +3

```
Query:    21 NHGGGCNSLLSIGNCLL 71
             N GG NSL SIG +L
Sbjct:    97 NMGGKTNSLSSIGKIVL 113
```

>Y57A10A.26 [Full Sequence]   [AceBrowser]  CE22631   (HINXTON)
        Length = 269

   Plus Strand HSPs:

  Score = 74 (26.0 bits), Expect = 0.016, P = 0.015
  Identities = 16/55 (29%), Positives = 28/55 (50%), Frame = +1

```
Query:     4 FFFWEEITAADATVFSQLAT-VYYP-FRNHISDVLEKDFPKLLEYCERVRHEVYP 162
             + F  I  D T F+ LA +Y P F  I  +++  P ++EY R++ + +P
Sbjct:   197 YLFGSSIKTIDVTAFAHLAELIYTPQFSPEIRAYIDEKVPNVMEYVIRIKEKYWP 251
```

>C14C11.8 [Full Sequence]   [AceBrowser]  CE06827   (ST.LOUIS)
        Length = 654

   Minus Strand HSPs:

```
Score = 43 (15.1 bits), Expect = 0.66, Sum P(2) = 0.48
Identities = 7/13 (53%), Positives = 7/13 (53%), Frame = -1

Query:     115 GSPFREHPKCDCG 77
               G P    P CDCG
Sbjct:     113 GCPSISSPSCDCG 125


Score = 41 (14.4 bits), Expect = 0.66, Sum P(2) = 0.48
Identities = 7/13 (53%), Positives = 9/13 (69%), Frame = -2

Query:      42 CCIRRRDFLPKKK 4
               CC+R+R  L K K
Sbjct:     641 CCLRKRHRLAKNK 653
```

```
>Y5H2B.4 [Full Sequence]   [AceBrowser]  CE21318   (ST.LOUIS)
         Length = 307

   Plus Strand HSPs:

 Score = 58 (20.4 bits), Expect = 1.0, P = 0.65
 Identities = 17/67 (25%), Positives = 31/67 (46%), Frame = +2

Query:    44 SSLNWQLSIIHSAITFRMFSKRTSQSYWSTVKE--FVMKFTQRTLL-CELNCQT-SSQIN 211
             S N++L+I +  +T        YW+T K    +++ F   +L C+L +   SQ N
Sbjct:   158 SFCNFRLNIPYGCVTLSCSLNLCFYQYWTTYKTIVYILTFLSTIVLTCKLLLKIHESQSN 217

Query:   212 KILRGKK 232
               + R +
Sbjct:   218 NLTRANR 224
```

```
>R13D7.7 [Full Sequence]   [AceBrowser]  CE18153   (ST.LOUIS)
         Length = 273

   Plus Strand HSPs:

 Score = 52 (18.3 bits), Expect = 1.1, Sum P(2) = 0.67
 Identities = 13/33 (39%), Positives = 20/33 (60%), Frame = +1

Query:    94 DVLEKDFPKLLEYCERVRHEVYPKDFTM*IKLS 192
             D++ K  P+ LE  E  + E++P DF +  KLS
Sbjct:   180 DMVNKTLPESLERLE-CQFEIHPGDFIIGNKLS 211

 Score = 34 (12.0 bits), Expect = 1.1, Sum P(2) = 0.67
 Identities = 6/8 (75%), Positives = 7/8 (87%), Frame = +3

Query:    12 LGGNHGGG 35
             LGG +GGG
Sbjct:    33 LGGYYGGG 40
```

```
>F58H7.5 [Full Sequence]   [AceBrowser]  CE17933   (ST.LOUIS)
         Length = 272

   Minus Strand HSPs:
```

```
    Score = 57 (20.1 bits), Expect = 1.1, P = 0.68
    Identities = 13/39 (33%), Positives = 19/39 (48%), Frame = -1

Query:   154 LHDELFHSTPITLGSPFREHPKCDCGMDNRQLPIERRLL 38
               L D L    P  +  PFRE P+ D  M   Q P+++  +
Sbjct:   143 LEDPLRRRVPYEIHFPFREPPQEDAPHRMAQNPVDQEAI 181




>Y41D4A.A [Full Sequence]  [AceBrowser]  CE21846    (ST.LOUIS)
             Length = 347

   Plus Strand HSPs:

   Score = 54 (19.0 bits), Expect = 1.3, Sum P(2) = 0.71
   Identities = 10/27 (37%), Positives = 18/27 (66%), Frame = +2

Query:   23 SRRRMQQSSLNWQLSIYHSAITFRMFS 103
             + R M  SS+NW L+++ ++ T  +FS
Sbjct:   89 THRIMSGSSINWYLAVLSASDTLILFS 115

   Score = 34 (12.0 bits), Expect = 1.3, Sum P(2) = 0.71
   Identities = 11/33 (33%), Positives = 17/33 (51%), Frame = +2

Query:   125 WS-TVKEFVMKFTQRTLLCELNCQTSSQINKILR 223
              W+ T+ +V+ FT   LL  LN   S + +  R
Sbjct:   244 WAYTIVMYVVPFT---LLIALNSMVLSAVRRSRR 274




>T02E9.1 [Full Sequence]  [AceBrowser]  CE13062   G-protein coupled receptor (HINXTON)
             Length = 376

   Plus Strand HSPs:

   Score = 58 (20.4 bits), Expect = 1.4, P = 0.74
   Identities = 17/53 (32%), Positives = 22/53 (41%), Frame = +2

Query:    83 ITFRMFSKRTS----QSYWSTVKEFVMKFTQRTLLCELNCQTSSQINKILRGKK 232
             +T RM  KRT      + Y   E  KF   L+C  +C+   I    GKK
Sbjct:   321 VTERMIRKRTKSMHEKGYSEAAVELTSKFDDVPLMCP-HCEAQLSIRSSSNGKK 373




>F32A5.2 [Full Sequence]  [AceBrowser]  CE01934   Peroxidase (ST.LOUIS)
             Length = 977

   Minus Strand HSPs:

   Score = 61 (21.5 bits), Expect = 2.0, P = 0.86
   Identities = 10/26 (38%), Positives = 16/26 (61%), Frame = -2

Query:    81 AEWIIDSCQLREDCCIRRRDFLPKKK 4
             A+W++D+CQL  + C R+     P K
Sbjct:    61 ADWMVDNCQLACNTCTRKNVIRPATK 86




>F23H12.5 [Full Sequence]  [AceBrowser]  CE05708   Thrombospondin type 1 domain (HINXTON
             Length = 802
```

Minus Strand HSPs:

Score = 48 (16.9 bits), Expect = 2.4, Sum P(2) = 0.91
Identities = 8/17 (47%), Positives = 11/17 (64%), Frame = -1

Query:  112 SPFREHPKCDCGMDNRQ 62
            SP+ E  KC CG  +R+
Sbjct:  707 SPWSEWTKCQCGKQSRK 723

Score = 32 (11.3 bits), Expect = 2.4, Sum P(2) = 0.91
Identities = 5/10 (50%), Positives = 7/10 (70%), Frame = -2

Query:  189 QFNSHSKVLW 160
            QF +  KV+W
Sbjct:  697 QFKNGKKVIW 706

>T04C9.4A [Full Sequence]  [AceBrowser]  CE26618    (ST.LOUIS)
            Length = 120

   Minus Strand HSPs:

 Score = 48 (16.9 bits), Expect = 2.8, P = 0.94
 Identities = 14/32 (43%), Positives = 16/32 (50%), Frame = -1

Query:  166 PLGKLHDELFHSTPITLGSPFR--EHPKCD-CG 77
            PL  L D  H+        PF+  EHPKC  CG
Sbjct:    9 PLSHLTDPA-HTIFKVSSMPFKPVEHPKCPKCG 40

>T02G5.9 [Full Sequence]  [AceBrowser]  CE04861    lysyl-tRNA synthetase (ST.LOUIS)
            Length = 572

   Plus Strand HSPs:

 Score = 56 (19.7 bits), Expect = 3.7, P = 0.98
 Identities = 11/25 (44%), Positives = 14/25 (56%), Frame = +3

Query:   39 NSLLSIGNCLLSIPQSHFGCSRKGL 113
            N +L + CL +P SHFG  K L
Sbjct:  180 NEILQLTPCLHMLPHSHFGLKDKEL 204

>T04C9.4B [Full Sequence]  [AceBrowser]  CE26619    (ST.LOUIS)
            Length = 138

   Minus Strand HSPs:

 Score = 48 (16.9 bits), Expect = 3.8, P = 0.98
 Identities = 14/32 (43%), Positives = 16/32 (50%), Frame = -1

Query:  166 PLGKLHDELFHSTPITLGSPFR--EHPKCD-CG 77
            PL  L D  H+        PF+  EHPKC  CG
Sbjct:    9 PLSHLTDPA-HTIFKVSSMPFKPVEHPKCPKCG 40

>W10G11.16 [Full Sequence]  [AceBrowser]  CE14830    channel protein (ST.LOUIS)

Length = 327

Minus Strand HSPs:

Score = 53 (18.7 bits), Expect = 4.0, P = 0.98
Identities = 12/33 (36%), Positives = 19/33 (57%), Frame = -2

Query:   165 LWVNFMTNS--FTVLQ*LWEVLFENIRNVIAEW 73
             LW  F+T    FT+LQ L+ + F+   N + +W
Sbjct:   230 LWFGFITGFVFFTLLQTLFVIGFDKRANQLKKW 262

>K10D3.2 [Full Sequence]    [AceBrowser]  CE25055  locus:unc-14   (HINXTON)
             Length = 665

  Minus Strand HSPs:

 Score = 56 (19.7 bits), Expect = 4.4, P = 0.99
 Identities = 11/31 (35%), Positives = 20/31 (64%), Frame = -2

Query:   111 VLFENIRNVIAEWIIDSCQLREDCCIRRRDF 19
             +LFE++   ++   +DS Q RE C +++ DF
Sbjct:   35 MLFESVDPSVSTDSLDSQQFRERCQMKKEDF 65

>F40G12.4 [Full Sequence]    [AceBrowser]  CE10182      (HINXTON)
             Length = 294

  Minus Strand HSPs:

 Score = 52 (18.3 bits), Expect = 4.4, P = 0.99
 Identities = 12/35 (34%), Positives = 20/35 (57%), Frame = -2

Query:   114 EVLFENIRNVIAEWIIDSCQLREDCCIRRRDFLPK 10
             E+L + +N   ++  +S L+E+ C R  DFL K
Sbjct:   27 EILSDRTKNCFFKFF-ESVLLKENSCSRNFDFLAK 60

>F59E12.5 [Full Sequence]    [AceBrowser]  CE11526      (ST.LOUIS)
             Length = 527

  Plus Strand HSPs:

 Score = 54 (19.0 bits), Expect = 5.5, P = 1.0
 Identities = 12/36 (33%), Positives = 16/36 (44%), Frame = +3

Query:     9 FLGCNHGGGCNSLLSIGNCLLSIPQSHFGCSRKGLP 116
             F G + GG   ++ S G+C          CS  GLP
Sbjct:   489 FSGSSSGGSRGAVWSCGHCTFQNEAGRQDCSMCGLP 524

>C08E3.8 [Full Sequence]    [AceBrowser]  CE08011      (ST.LOUIS)
             Length = 431

  Minus Strand HSPs:

 Score = 53 (18.7 bits), Expect = 5.6, P = 1.0

Identities = 8/12 (66%), Positives = 9/12 (75%), Frame = -1

```
Query:    112 SPFREHPKCDCG 77
              SPFR+ P C CG
Sbjct:    147 SPFRQEPTCTCG 158
```

>F11G11.3 [Full Sequence]  [AceBrowser]  CE07056   Glutathione S-transferase (ST.LOUIS)
         Length = 235

  Plus Strand HSPs:

 Score = 55 (19.4 bits), Expect = 6.1, P = 1.0
 Identities = 15/52 (28%), Positives = 27/52 (51%), Frame = +1

```
Query:      4 FPFWEEITAADATVF---SQLATVYYPFRNHISDVLEKDFPKLLEYCERVRH 150
              F F+E I A++ + F   + L V      H+ D+L+KD   + E+ + + H
Sbjct:    162 FEFFENILASNHSGFFVGNSLTWVDLLISQHVQDILDKDLAVVEEFKKVLAH 213
```

>C46E10.9 [Full Sequence]  [AceBrowser]  CE08767   zinc finger protein (ST.LOUIS)
         Length = 416

  Minus Strand HSPs:

 Score = 52 (18.3 bits), Expect = 6.8, P = 1.0
 Identities = 12/41 (29%), Positives = 19/41 (46%), Frame = -1

```
Query:    154 LHDELFHST-PITLGSPFREHPKCDCGMDNRQLPIERRLLH 35
              +H   +HST P L +P +E   C   D+ + +    LH
Sbjct:    341 IHHYYYHSTNPAQLQNPAQECQHCKIQFDDAPMSLLHNALH 381
```

>T04C9.4C [Full Sequence]  [AceBrowser]  CE26620   contains LIM-like binding domain (ST.
         Length = 206

  Minus Strand HSPs:

 Score = 48 (16.9 bits), Expect = 7.4, P = 1.0
 Identities = 14/32 (43%), Positives = 16/32 (50%), Frame = -1

```
Query:    166 PLGKLHDELFHSTPITLGSPFR--EHPKCD-CG 77
              PL  L D  H+      PF+  EHPKC  CG
Sbjct:      9 PLSHLTDPA-HTIFKVSSMPFKPVEHPKCPKCG 40
```

>Y22D7AR.3 [Full Sequence]  [AceBrowser]  CE23432   (ST.LOUIS)
         Length = 65

  Plus Strand HSPs:

 Score = 45 (15.8 bits), Expect = 7.9, P = 1.0
 Identities = 7/17 (41%), Positives = 13/17 (76%), Frame = +1

```
Query:    115 PKLLEYCERVRHEVYPK 165
              P++++YC R+ H + PK
Sbjct:     29 PRIIDYCTRIFH-LSPK 44
```

>F52A8.1 [Full Sequence]   [AceBrowser]  CE05908    (HINXTON)
          Length = 110

  Minus Strand HSPs:

 Score = 46 (16.2 bits), Expect = 8.1, P = 1.0
 Identities = 7/21 (33%), Positives = 12/21 (57%), Frame = -2

Query:   75 WIIDSC-QLREDCCIRRRDFL 16
            W    C Q+ + CC R +D++
Sbjct:   64 WYFKCCGQIADQCCFRLQDWV 84


>ZK1037.6 [Full Sequence]  [AceBrowser]  CE16758    (HINXTON)
          Length = 491

  Minus Strand HSPs:

 Score = 52 (18.3 bits), Expect = 8.3, P = 1.0
 Identities = 11/22 (50%), Positives = 15/22 (68%), Frame = -2

Query:  105 FENIRNVIAEWIIDSCQLREDC 40
            +EN +N IA +   SCQ+ RDC
Sbjct:  244 YENTKN-IASFQSISCQIMRDC 264


Parameters:
  P=4
  warnings
  B=100
  filter=seg
  V=100
  C=1 (Standard genetic code)

  ctxfactor=5.39
  E=10

| Query Frame | MatID | Matrix name | ----- As Used ----- | | | ----- Computed ---- | | |
|---|---|---|---|---|---|---|---|---|
| | | | Lambda | K | H | Lambda | K | H |
| Std. | 0 | BLOSUM62 | | | | 0.318 | 0.135 | 0.401 |
| +3 | 0 | BLOSUM62 | 0.318 | 0.135 | 0.401 | 0.341 | 0.158 | 0.521 |
| | | q=9  r=2 | 0.244 | 0.0300 | 0.180 | | | |
| +2 | 0 | BLOSUM62 | 0.318 | 0.135 | 0.401 | 0.328 | 0.132 | 0.393 |
| | | q=9  r=2 | 0.244 | 0.0300 | 0.180 | | | |
| +1 | 0 | BLOSUM62 | 0.318 | 0.135 | 0.401 | 0.350 | 0.153 | 0.537 |
| | | q=9  r=2 | 0.244 | 0.0300 | 0.180 | | | |
| -1 | 0 | BLOSUM62 | 0.318 | 0.135 | 0.401 | 0.339 | 0.154 | 0.537 |
| | | q=9  r=2 | 0.244 | 0.0300 | 0.180 | | | |
| -2 | 0 | BLOSUM62 | 0.318 | 0.135 | 0.401 | 0.345 | 0.149 | 0.533 |
| | | q=9  r=2 | 0.244 | 0.0300 | 0.180 | | | |
| -3 | 0 | BLOSUM62 | 0.318 | 0.135 | 0.401 | 0.381 | 0.170 | 0.592 |
| | | q=9  r=2 | 0.244 | 0.0300 | 0.180 | | | |

| Query Frame | MatID | Length | Eff.Length | E | S | W | T | X | E2 | S2 |
|---|---|---|---|---|---|---|---|---|---|---|
| +3 | 0 | 78 | 73 | 10. | 51 | 3 | 12 | 22 | 0.095 | 31 |
| | | | | | | | | 27 | 0.12 | 31 |

| +2 | 0 | 79 | 79 | 10. 53 3 | 12 22 | 0.11 31 |
|  |  |  |  |  | 27 | 0.11 32 |
| +1 | 0 | 79 | 79 | 10. 53 3 | 12 22 | 0.11 31 |
|  |  |  |  |  | 27 | 0.11 32 |
| -1 | 0 | 79 | 52 | 10. 45 3 | 12 22 | 0.11 29 |
|  |  |  |  |  | 26 | 0.084 29 |
| -2 | 0 | 79 | 65 | 10. 47 3 | 12 22 | 0.11 30 |
|  |  |  |  |  | 27 | 0.092 31 |
| -3 | 0 | 78 | 78 | 10. 53 3 | 12 22 | 0.10 31 |
|  |  |  |  |  | 27 | 0.11 32 |

Statistics:

Database:  /data/blastdb/wormpub/wormpep_current
   Title:  wormpub/wormpep_current
   Release date:  unknown
   Posted date:  12:07 PM BST Apr 24, 2001
   Format:  BLAST
# of letters in database:  8,675,472
# of sequences in database:  19,835
# of database sequences satisfying E:  33
No. of states in DFA:  581 (114 KB)
Total size of DFA:  253 KB (256 KB)
Time to generate neighborhood:  0.00u 0.01s 0.01t  Elapsed: 00:00:00
No. of threads or processors used:  4
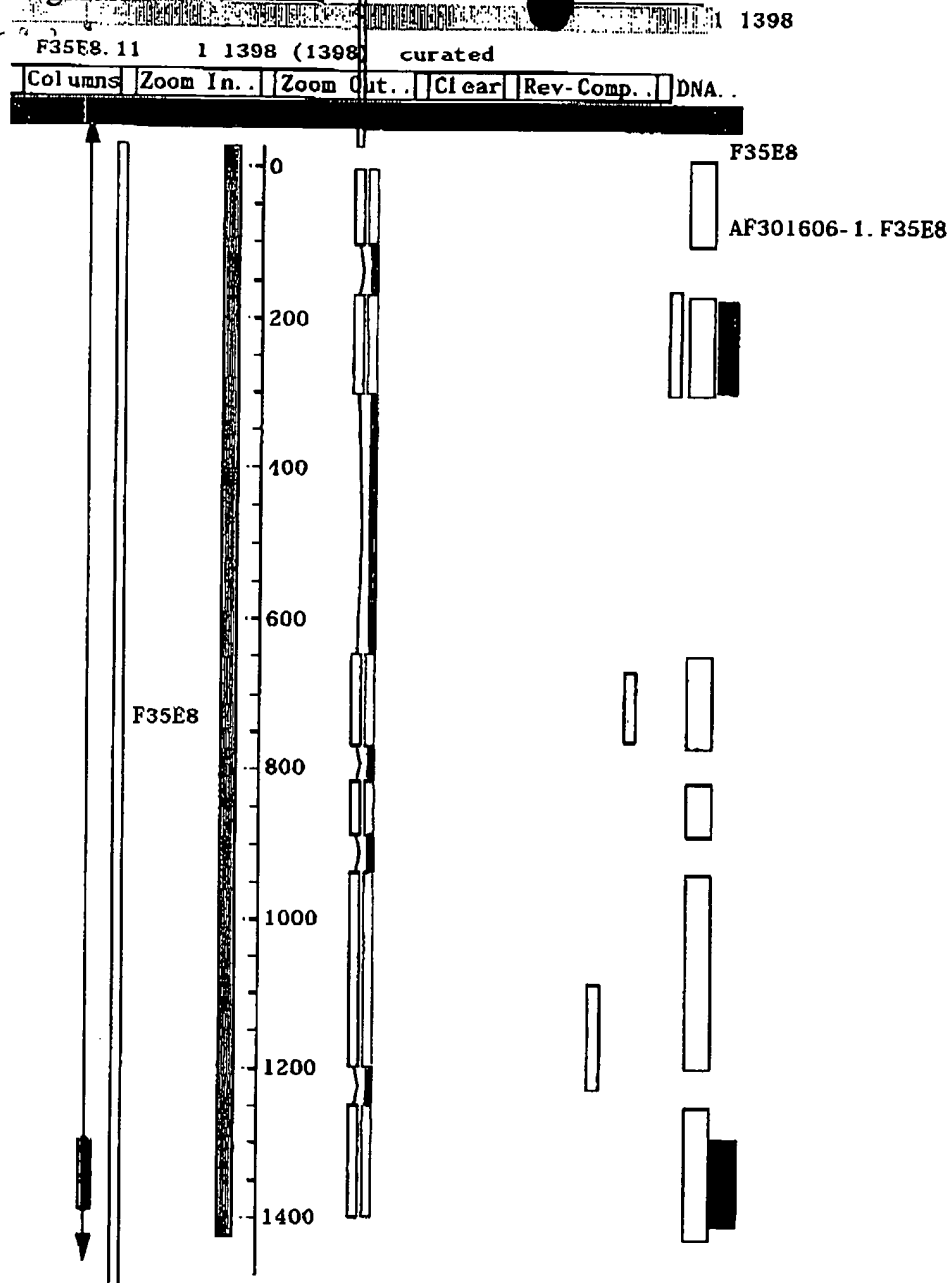Search cpu time:  5.55u 0.65s 6.20t  Elapsed: 00:00:17
Total cpu time:  5.66u 0.86s 6.53t  Elapsed: 00:00:24
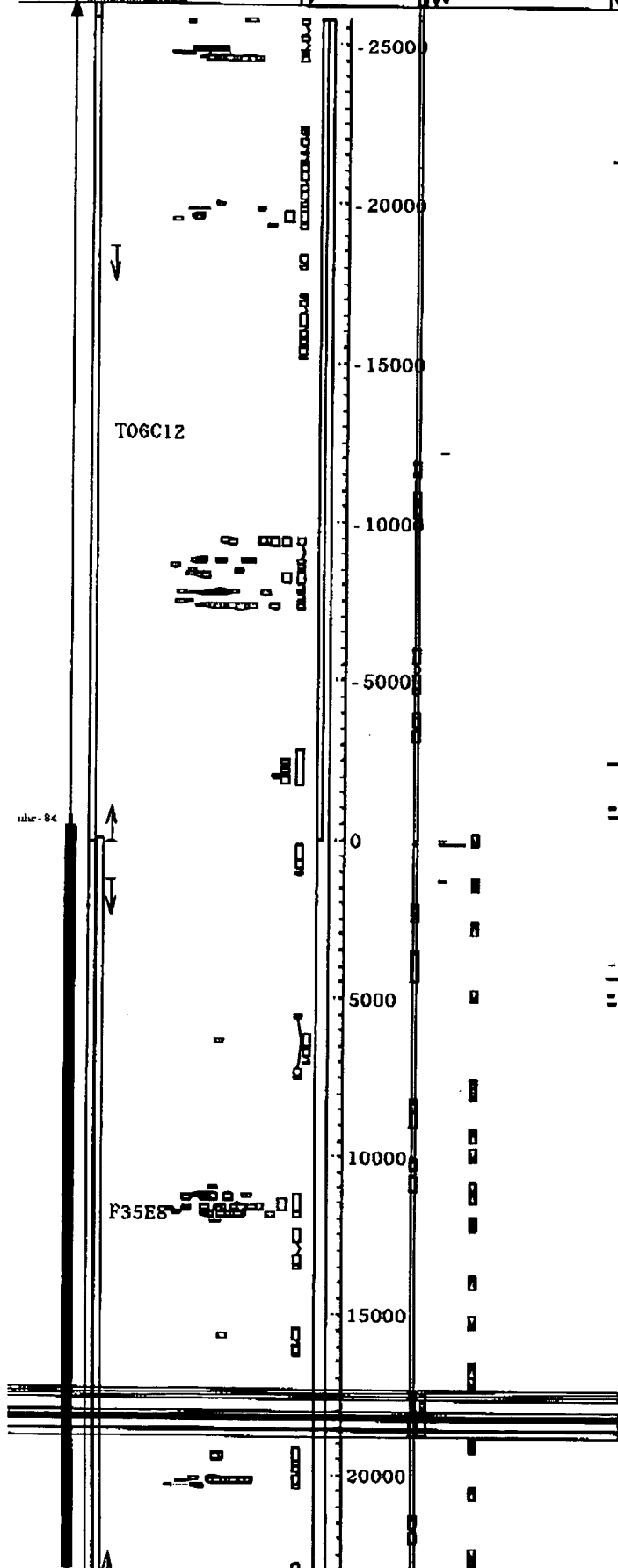Start:  Thu May 17 17:05:07 2001   End:  Thu May 17 17:05:31 2001

ript last modified Mon Apr 23 17:35:41 2001                                      webmaster@sanger.ac.uk

Figure 6



F35E8. 11        1   1398  (1398)      curated

Columns | Zoom In.. | Zoom Out.. | Clear | Rev-Comp.. | DNA..

AF301606-1. F35E8          17378  18775   (1398)     NDB_CDS

Column Zoom In Zoom Out Clear Rev Comp DNA Analysis..

- 2500

- 2000

- 1500

T06C12

- 1000

- 5000

0

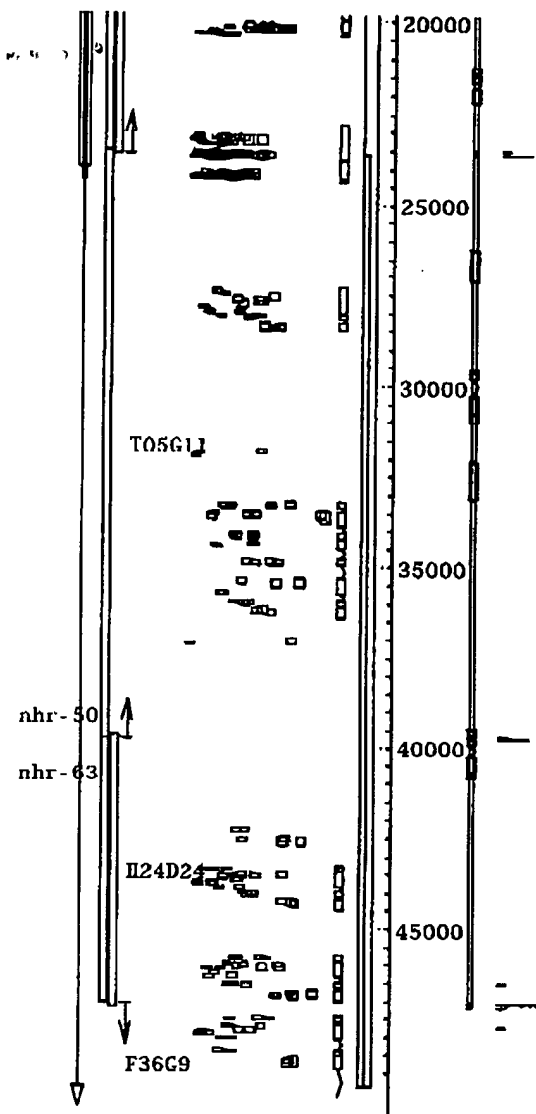unc-84

5000

10000

F35E8

15000

20000

Figure 7

>F35E8.11 Glutathione S-transferases.
atgttggattcatgtttgattattactgctgcgctgtttggagccgctgt
catttacttgaaaaatttcttcactgttcctagcattaaaccaaaacctg
atattcacaaaaaagactacaaaaaggatgtagtctatctgtatcagatg
aagagactcaagaactgtccgaacttgtcccctttctgcatgaaaatcga
gattctttgtagaatcttcaagattccttacgagattatcacatgcacct
ctgaacgctctcggaatggattggtccctttcgttgaactcaatggagag
cacattgctgattctgatcttatcgaaatgcgcttgagatcacattttaa
aattccgtcgcttccaactgagctggaaactcaatctgttgctctaagca
agtttgcagatcaccatttgttcttcgtacttatacgatttaaaattgct
gtcgacgaattctacaaaaccattattgaaataatcggtctcccaacctt
cctgaatttccttctcatgccccttttgaaggctataatcgggaaaaatg
tctacaacaaatgtcagggagccattggagattttgaattgagtgagctc
gacgagattcttcacagagatttgcgaatcgtagagaacaccttggccaa
gaaaaagtttcttttcggggaggaaatcacggcggcggatgcaacagtct
tctctcaattggcaactgtctattatccattccgcaatcacatttcggat
gttctcgaaaggacttcccaaagttattggagtactgtgaaagagttcg
tcatgaagtttacccaaaggactttactatgtga

Figure 8

>F35E8.11 Glutathione S-transferases.
MLDSCLIITAALFGAAVIYLKNFFTVPSIKPKPDIHKKDYKKDVVYLYQM
KRLKNCPNLSPFCMKIEILCRIFKIPYEIITCTSERSRNGLVPFVELNGE
HIADSDLIEMRLRSHFKIPSLPTELETQSVALSKFADHHLFFVLIRFKIA
VDEFYKTIIEIIGLPTFLNFLLMPLLKAIIGKNVYNKCQGAICDFELSEL
DEILHRDLRIVENTLAKKKFLFGEEITAADATVFSQLATVYYPFRNHISD
VLEKDFPKLLEYCERVRHEVYPKDFTM*